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3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

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	E 201 V 1913	- 170 A 1853	- 133 F 1793	Y 78 - 1742	10;			10710, A 2, Appli 5, Appli 6, Appli 15, Appl 15, Appl 15, Appl 15, Appl 162, Appl 162, Appl 15, Appl 15, Appl 15, Appl 16, Appli 15, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 16, Appli 17, Appli 17, Appli 17, Appli 18, Appli 19, Appli 19, Appli 19, Appli

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GENERAL INFORMATION:
APPLICANT: Hitachi, Ltd.
TITLE OF INVENTION: AIP1-INTERACTING PROTEINS AND USE
FILE REFERENCE: HITA.0164
CURRENT APPLICATION NUMBER: US/10/370,481
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/358,369
PRIOR FILING DATE: 2002-02-22
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CURRENT APPLICATION NUMBER: PCT/US03/19834
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 10/445,724
PRIOR PILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: 60/392,158
PRIOR APPLICATION NUMBER: 60/392,158
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEO ID NOS: 3
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PRIOR FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 50
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TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS
TITLE OF INVENTION: METHODS FOR TREATING HYPERLIPIDEMIA
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TYPE: PRT
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active 65; Mismatches
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Best Local Similarity
Matches 73; Conserv
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LENGTH: 4574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saunders, Michael John Scott
APPLICANT: Logghe, Marc Georges
TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the
TITLE OF INVENTION: prevention and/or treatment of metabolic diseases and nucleor
TITLE OF INVENTION: sequences encoding such amino acid sequences.

FILE REFERENCE: D00590.70042.US
CURRENT FILLING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 526
SOFTWARE: PatentIn version 3.2
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2281 LILROKONTORFLOEEAEKMKOVAEEAARLSVAAQEAARLROLAEEDLAQORALAEKMLK 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2013 AEERVQKSLAAEEEAARQRKAALEEVERLKANVEEARRLRERAEQESARQLQLAQEAAQK
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                                                                                                                                                                                                                                                                                                                               113 VSPAHYVPESDASQAAPYIEQAQVIAHQFKEKVLAFA-SRGNHDSPTHYVPESDAKPAII 171
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                                                                                                                                                                                                                                                                                                                                                                                                                             56 AEQFKQKALAFASRQNHVSPTHYVPESDARPAIIPDREVLHREFDEME-EAFASR--GNH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AEQFKQKAL-----RPAVIPDREVL-----YQEFDEMEEASHLPYIEQGMQL
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                                          FASRGNHVSPRHYVPESEPQVVVTPDKEILYEAFDE---MEEASKAALIEEGQRMAEMLK 348
                                                                                                                                          LVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQFKEKVLA
                                                                                                                                                                                         EQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTTLRLQ----
                                                                                                                                                                                                                                   PDREVLYREFDEMEESQHLPYIEQGMMLAEQFKQKALAFASRGNHVAPTHYVTESDAKPA
                                                                                                                                                                                                                                                                                     AEEARVQAEREAAQARRQVEEAERLKQSAEEQAQARAQAQAAAEKLRKEAEQEAARRAQA 2179
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20.1%; Pred. No. 0.13;
                                                                                           DEELQRLKAEATEAARQRSQVEEELFSVRVQMEELSKLKARIEAENRA
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                                                                                                                                                                                         -LEETDHQKN 2230
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US-60-479-073-506; Sequence 506, Application US/60479073; GENERAL INFORMATION:
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US-60-479-073-497
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NUMBER OF SEQ ID NOS: 526
SOFTWARE: PatentIn version 3.2
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FILE REFERENCE: D00590.70042.US
CURRENT APPLICATION NUMBER: US/60/479,073
CURRENT FILING DATE: 2003-66-17
                                                                                                                      APPLICANT: Saunders, Michael John Scott
"TCANT: Logghe, Marc Georges
                                                                                                                                                     APPLICANT: De Wilde, Gert Jules Hector
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TITLE OF INVENTION: Amino acid sequences useful for developing compound
TITLE OF INVENTION: prevention and/or treatment of metabolic diseases
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                                                                                   ""Logghe, Marc Georges
"TNVENTION: Amino acid so
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                                                                               Amino acid sequences useful for developing compounds prevention and/or treatment of metabolic diseases ar
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                           sequences encoding such amino acid sequences.
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Pred. No. 0.13;
3; Mismatches 176;
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; ORGANISM: Homo sapiens US-10-273-573-10712
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                                                                                                                                                                                                                                                                                                                              SEQ ID NO 10712
LENGTH: 365
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SOFTWARE: PatentIn version
SEQ ID NO 506
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TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                    Local
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                                         123 DASQAAPYIEQAQVIAHQFKE---KVLAFASRGNHDSPTHYVPESDAKPAIIPDREVLYR 179
    48
                                                                                                                                69 RONHVSPTHYVPESDAR-----PAIIPDREVLHREFDEMEEAFASRGNHVSPAHYVPES 122
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                                                                                                                                                                                                  Similarity
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19.7%; Pred. No. 0.13;
-YVSHKHSELHSRVLESYVRDKHSEPSSSVLES-----YVRDK-----
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Pred. No. 0.016;
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US-60-479-073-498
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SEQ ID NO 498
LENGTH: 5373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the TITLE OF INVENTION: prevention and/or treatment of metabolic diseases and nucleotide TITLE OF INVENTION: sequences encoding such amino acid sequences. FILE REFERENCE: D00590.70042.US CURRENT APPLICATION NUMBER: US/60/479,073 CURRENT FILING DATE: 2003-06-17 NUMBER OF SEQ ID NOS: 526
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APPLICANT: Saunders, Michael John Scott
APPLICANT: Logghe, Marc Georges
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ORGANISM: Homo sapiens
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                                                                          EPMLETLENLSSRLRMP---PLIPAEVDK--IRECISDNKSAT--VELEKLQPSFEALKR 3939
                                     K 350
                                                                                                                                                                                                          ALVPDK-EVLYQQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQFKEKV 289
                                                                                                                                                                                                                                                         QLRQQQEEMRQLRESIAEHKPHIDKLLKIGPQLKE--
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                                                                                                                      LAFASRGNHVSPRHYVPESEPQVVVTPDKEILYEAFDEMEEASKAALIEEGQRMAEMLKS 349
                                                                                                                                                                   -LNPEEGEMVEEKYQKAENMYAQIKEEVRQRALALDEAVSQSTQIT-----EFHDKI 3886
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18.5%; Pred. No. 1.4;
ative 73; Mismatches 132;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-479-073-500
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                                                                                                                                                                                   Sequence 10, Application US/10333120A GENERAL INFORMATION:
APPLICANT: Janulczyk, Robert
APPLICANT: Januelli, Francesco
APPLICANT: Sjoholm, Anders
APPLICANT: Bozzi, Gianni
APPLICANT: Bjorck, Lars
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 13519PCTUS
CURRENT APPLICATION NUMBER: US/10/333,120A
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CURRENT FILING DATE: 2003-06-17
NUMBER OF SEQ ID NOS: 526
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APPLICANT: Saunders, Michael John Scott
APPLICANT: Logghe, Marc Georges
TITLE OF INVENTION: Amino acid sequences useful for developing compounds for the
TITLE OF INVENTION: prevention and/or treatment of metabolic diseases and nucle
TITLE OF INVENTION: sequences encoding such amino acid sequences.
FILE REFERENCE: D00590.70042.US
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RESULT 11
US-10-391-363A-61
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                                                                                                                                                                                                                                                                                                    SEQ ID NO 61
LENGTH: 970
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                     -10-391-363A-61
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/365,202
PRIOR FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: REN-02-052 MON-52933
CURRENT APPLICATION NUMBER: US/10/391,363A
CURRENT FILING DATE: 2003-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Monsanto Technology LLC
APPLICANT: Valentin, Henry E
APPLICANT: Venkatesh, Tyamagondlu V
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Homogentisate Prenyl Transferase ("HPT") Nucleic Acids and Polype
TITLE OF INVENTION: and Uses Thereof
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PRIOR APPLICATION NUMBER: PCT/EP01/08409
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: SE 0002728-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 693
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                Local Similarity
les 72; Conserv
                 Zu<sub>Z</sub>
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                                                                                                                                                  31 EVLYQEFDEMEEASHLPYIEQGM------QLAEQFKQKALAFASRQNHVSPTHYVP 80
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                                                                                                          VQQHHLDNV--SSHLMYİLRSIYKEASLDDLKPRAEQIQQLSTRLSEARNARSLTNLVK 323
                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                5.2%; Score 95; DB 6
21.4%; Pred. No. 0.62;
                                                                  PPAIIPDREVLHREFDE---MEEAFASRGNHVS------PAHYVPE 121
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22.0%;
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Pred. No. 0.38;
                        ~¬KPENTEKKALEEAEIKEKPETSNLKAVTLEQTAREAPE
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PCT-US02-18638A-6
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APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035PC
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.2%;
Best Local Similarity 19.3%;
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PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 3907
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                                       VSPRHYVPESEPQVVVTPDKEILYEAFDEM---EEASKAALIEEGQRMAEMLK 348
                                                                                EQLEQFREELENKNEEVQQLHMQLEIQKKESTTRLQELEQENKLFKDDMEKLGLAIK---
                                                                                                                         QQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQFKEKV--LAFASRGNH
                                                                                                                                                              EFRVRELEQALLVSADTFOKVEDRKHFGAVEAKPELSLEVOLQAERDAIDRKEKEITNLE
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ESDAMSTQDQHVLFGKFAQIIQEKEVEIDQLNEQVTKLQQQLK
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Pred. No. 4.6;
4; Mismatches 145; Indels
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
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                                                                                                              SOFTWARE: Custom SEQ ID NO 9038
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                                                                                                                                                             APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR PILING DATE: 2000-01-26
PRIOR PILING DATE: 2000-01-26
NUMBER: 09/522,929
PRIOR FILING DATE: 2000-01-26
NUMBER: 09/520,160
PRIOR FILING DATE: 2001-01-26
NUMBER: 09/520,160
PRIOR FILING DATE: 2001-01-26
NUMBER: 09/520,160
PRIOR FILING DATE: 2001-01-26
NUMBER: 09/520,160
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
                       FEATURE
                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFRVRELEQALLVSADTFQKVEDRKHFGAVEAKPELSLEVQLQAERDAIDRKEKEITNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMLAEQFKQKALAFASRGNHVAPTHYVTESDAKPALV------PDKEV--LY 240
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19.3%;
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530 LKQQAKEKQAQ---

Similarity

61;

Mismatches

141;

Indels 85;

Gaps

17;

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13 LAEQFKQKALRPAVIPDREVLYQEFDEMEEASHLPYIEQGM-----QLAEQFKQKALAF-

-LAQTLQQQEQAS-----QGLRHQVEQLSSSLKQKEQQLK 574

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US-10-273-573-9034
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GENERAL INFORMATION:
                     Query Match
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                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 21272-066
CURRENT APPLICATION NUMBER: US/10/273,573
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: 09/522,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 10994
SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS
                                                                               NAME/KEY: DOMAIN
LOCATION: (2097)..(2112)
OTHER INFORMATION: POLLEN ALLERGEN POA PI SIGNATURE domain identified by
OTHER INFORMATION: eMATRIX, accession number PR00833H, p-value=3.077e-09,
OTHER INFORMATION: 2.30
                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (2093)..(2108)
OTHER INFORMATION: POLLEN ALLERGEN POA PI SIGNATURE domain identified by OTHER INFORMATION: EMATRIX, accession number PR00833H, p-value=3.077e-09, OTHER INFORMATION: 2.30
                                                                                                                                                                                                                                                      ENGTH: 2121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 EVAEKQEATRODHAQ--QLATAAEEREASLRERDAALKQLEALEKEKAAKLEILQQQLQV 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANEARDSAQTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQQK 686
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b; Pred. No. 2.1;
61; Mismatches 141;
  Score 94.5;
Pred. No. 2
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                     DB
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                   Length 2121,
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575 EVAEKQEATRQDHAQQLATAAEERBASLRERDAALKQLEALEKEKÄAKLEILQQQLQV 632 120 PESDASQAAPYIEQAQVIAHQFKEKVLAFASRGNHDSPTHYVPESDAKP 168 633 ANEARDSAQTSVTQAQREKAELSRKVEELQACVETARQEQHEAQAQVAELELQLRSEQQK 692 169 ALIPDREVLYREFDEMEESQHLPYIEQGMMLAEQFKQKALAFASRGNHVAPTHYV 223 1	ASRQNHVSPTHYVPESDARPAIIPDREVL

Search completed: July 25, 2003, 13:20:07 . Job time : 15 secs

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Minimum
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                                                                  Query
                                                                                                                                                                                                                                                                                         5580241 seqs, 870357830 residues
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Gapop 10.0 , Gapext 0.5
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/ Cgn2 6/ptcdata/1/paa/US08_COMB.pep: *
/ Cgn2 6/ptcdata/1/paa/US081_COMB.pep: *
/ Cgn2 6/ptcdata/1/paa/US081_COMB.pep: *
/ Cgn2 6/ptcdata/1/paa/US084_COMB.pep: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | cgn2_6/prod== AA_Main:*
           18 US-09-491-146-52
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                                                                         Description
       Sequence 52,
Sequence 52,
                                                                                                                                                                                                                                                                                                RESULT 1
US-09-491-146-52
; Sequence 52, Application US/09491146
; GENERAL INFORMATION:
APPLICANT: KHUDYAKOV, YURI E.
FIELDS, HOWARD A.
TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
MOSAIC PROTEIN AND RESTRICTION METHOD FOR MAKING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: GA

COUNTRY: USA

ZIF: 30303-1769

ZIF: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/491,146

FILING DATE: 25-Jan-2000
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STREET: 191 Peachtree Street, N.W., 37th Floor
CLASSIFICATION: <Unknown:
                                                                                                                                                                                                                                                                             CITY: Atlanta
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US-07-769-996E-12

US-07-769-996E-12

US-08-099-706-12

US-08-099-706-32

US-08-099-706-32

US-07-769-996E-3

US-07-769-996E-3

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US-09-711-84-150-3

US-09-721-898-3

US-09-963-433-2

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US-08-403-590B-30

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US-08-403-590B-30

US-09-721-479B-1
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US-08-417-478-1
US-08-453-613-1
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US-09-791-537-91118
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Sequence 5, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 32, Appli Sequence 34, Appli Sequence 36, Appli Sequence 36, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appli Sequence 2, Appli Sequence 14, Appli Sequence 14, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 3, Appli Sequence 4, Appli

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APPLICANT: The Government of the United States of America, as represent APPLICANT: the Secretary, Department of Health and Human Services, APPLICANT: the Secretary Disease Control and Prevention APPLICANT: Khudyakov, Yury APPLICANT: Fields, Howard TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION ENDONUCLEASE ASSISTE TITLE OF INVENTION: LIGATION METHOD FOR MAKING THE SAME FILE REFERENCE: 14114.0344U2 CURRENT APPLICATION NUMBER: US/09/491,146A CURRENT FILING DATE: 2000-01-25 PRIOR APPLICATION NUMBER: 08/921,887 PRIOR APPLICATION NUMBER: 08/921,887 PRIOR FILING DATE: 25-08-97 NUMBER OF SEQ ID NOS: 55 SOFTWARE: FASSEEQ for Windows Version 4.0 SEQ ID NO 52
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                                                                                                                                                                                                                                                                             Sequence 52, Application US/09491146A GENERAL INFORMATION:
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Best Local 9
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INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: Not Relevant TOPOLOGY: Not Relevant MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO FRACMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Hepatitis virus SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/921,887
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 03063-0380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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; OTHER INFORMATION: Description of Artificial Sequence: 
US-09-881-239-5
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                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 829
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application:
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: HCV ANTIGEN/ANTIBODY COMBINATION FILE REFERENCE: 2302-16073 / PP16073.003 CURRENT APPLICATION NUMBER: US/09/881,239 CURRENT FILING DATE: 2001-06-14 NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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APPLICANT: MEDINA-SELBY, Angelica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHIEN David Y.
APPLICANT: ARCANGEL, Phillip
APPLICANT: TANUBEKE, Laura
APPLICANT: GEORGE-NASCIEMENTO, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Hepatitis
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                                                                                                     226 SDAKPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQF
                                                                                                                                                                               167 KPAIIPDREVLYREFDEMEE-SQHLPYIEQGMMLAEQFKQKALAFASRGNHVAPTHYVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09881239
                            KEKVLAFASRGNHVSPRHYVPESEPQVVVTPDKEILYEAFDEMEE-ASKAALIEEGQRMA
                                                                     --GKPAIVPDKEVLYQQYDEMEE-
                                                                                                                                            KPAIIPDREVLYREFDEMEECSQHLPYIEQGMMLAEQFKQKALGL-SRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQFKEKVLAFASRGNHVS
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                                                                                                                                                                                                                     Conservative
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Pred. No. 6.8e-37;
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-DNDQVVVTPDKEILYEAFDEMEECASKAALIEEGQRMA
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                                                                     -CSQAAPYIEQAQVIAHQF
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TYPE: PRT
; ORGANISM: Synthetic construct
US-09-791-537-91118
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Mon Jul 28 11...
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 91118
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09881654
GENERAL INFORMATION:
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                                                                                                                                                                               APPLICANT: COLT, Doris
APPLICANT: MEDINA-SELBY, Angelica
TITLE OF INVENTION: IMMUNOASSAYS FOR ANTI-HCV ANTIBODIES
FILE REFERENCE: 2302-17039 / PP17039.002
CURRENT APPLICATION NUMBER: US/09/881,654
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/212,082
PRIOR FILING DATE: 2000-06-15
                                                                                                                                                                                                                                                                                              APPLICANT: CHIEN, David Y.
APPLICANT: ARCANGEL, Phillip
APPLICANT: TANDESKE, Laura
APPLICANT: GEORGE-NASCIEMENTO
APPLICANT: COLT, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bionomix, Inc.
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                                                                                 FILING DATE: 2001-04-02
APPLICATION NUMBER: 60/280,867
""G DATE: 2001-04-02
""NOS: 7
NOS: 7
2.0
                                                                                                                                                                  APPLICATION NUMBER: 60/280,811
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Pred. No. 6.9e-37;
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; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: MEFA 7.1 US-09-881-654-4
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Best Local Similarity
Matches 118; Conserv
                                                                    INFORMATION FOR SEQ ID NO: 1:
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                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      APPLICATION NUMBER: US 07 FILING DATE: 01-JAN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                           REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 51
   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                    LENGTH:
                                                                                                       TELEPHONE:
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                                    3011 amino acids
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ZECK, BILLY J.
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Pred. No. 1.1e-36;
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GENERAL INFORMATI
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release.#1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,613
FILING DATE:
                                                                      TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                      REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION: 708-937-6365
 MOLECULE TYPE:
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF INVENTION: PROTEINS
                TOPOLOGY:
                             STRANDEDNESS:
                                                                                                                                                               NAME: POREMBSKI, PRISCILLA E. REGISTRATION NUMBER: 33,207
                                                                                                                                                                                                                                                                                                                                                            ZIP: 60064-3500
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                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ABBOTT PARK
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les 87; Conserv
                                                            ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T: DEVARE; SUSHIL G.
INVENTION: MAMMALIAN EXPRESSION
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                                                            3011 amino acids
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DESAI, SURESH M.
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ZECK, BILLY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAMAGUCHI, JULIE
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protein
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Pred. No. 8.9e-13
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                                                                                                                                                                                                                                                                                Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74;
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                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local S
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY I
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 492
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                                                                                                                                                                         134 -AQVIAHQFKEKVLAF-----
                                                                                                                                                                                                            294
465 QWMNRLIAFASRGNHVSPTHYVPESDA 491
                                                                                                                                                                                                                                                                              242 KPAIIPDREVLYQEFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQTASRQ-----
                                                                                                                                                                                                                                                                                                           23 RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
                                                                                                                                                                                                                                             79 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
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Similarity 32.5%;
                                 QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                  GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV
                                                                                                                                      TAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGRVGLGKVLVDILA
                                                                                                                                                                                                          ----AEAITP---AVQTNWQRLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 344
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                                                                                                     -----PDREVLYREFDEMEESQHL--PYIEQGMML------
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Pred. No. 6.4e-14;
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RESULT 9 US-07-635-451-10

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US-07-635-451-10
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INFORMATION FOR SEQ ID NO: 10:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 31-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19901228
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC CINCENTION: CDNA AND ANTIGEN POLYPEPTIDE
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                                                                                                              ~44 TASITSPLTTQSTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA 1853
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                                                                                                                                                                                                                                                                      23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (202) 887-0357
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TAKAMIZAWA, Akahisa
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                                                                    -IPDREVLYREFDEMEESQHL--PYIEQGMML-------
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Pred. No. 5.8e-13;
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US-07-769-996B-12
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SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amin
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                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 659-2930
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                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
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CLASSIFICATION:
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                                                          79 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ---- 133
                                                                                                           23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
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                                                                                         RPAIVPDRELLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
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                                                                                                                                                                Conservative
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TAKAMIZAWA, Akahisa
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SYSTEM: PC-DOS/MS-DOS
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Kubovcik & Murray
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09-NOV-1990
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                            -VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                                                                                                                              31;
                                                                                                                                                                          Score 256; DB 3;
Pred. No. 5.8e-13;
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                                                                                                                                                              Mismatches
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Length 2013; Indels

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                      Query Match
Best Local Similarity
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amino acids
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APPLICATION NUMBER: JP 2-3
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2
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                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 28-DEC-1990
TTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                      TELEFAX:
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                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                  NAME: McLeland, Le-Nhung REGISTRATION NUMBER: 31,
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    14.1%; Score 256; DB 3; Length 2013; ilarity 31.1%; Pred. No. 5.8e-13; Conservative 31; Mismatches 75; Indels 7
                                                                                                                                                                                                                                        (202) 887-0357
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31-AUG-1990
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US-08-099-706-12
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          REFERENCE/DOCKET NUMBER: 31,404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2020
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                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 02-OCT-1991 ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS.DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
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CITY: Washington
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FILING DATE: 31-AUG-1990
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ADDRESSEE: Kubovcik & Murray
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                                                                                             O'Toole, J. Herbert
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MORI, Chisato
TAKAMIZAWA, Akahisa
  (202) 887-0357
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09-NOV-1990
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Mon Jul 28 11:16.74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08383682 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                       APPLICATION.
APPLICATION.
FILING DATE: 25-
POPLICATION NUMBER: JF
PATE: 25-JUN-1990
TON DATA:
JP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/720,961
APPLICATION NUMBER: 25-JUN-1991
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS PARTICLES NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS LENGTH: 2013 amino ac:
                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1725 K St
CITY: Washington
                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1914 QWMNRLIAFASRGNHVSPTHYVPESDA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1854 GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------ 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IPDREVLYREFDEMEESQHL--PYIEQGMML---
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                                                                                                                                                                                                                                                                                                                                                                                                     E: Murray
1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOSHIDA, Iwao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAKAMIZAWA, Akahisa
                                                                                                                                                                                                                                                                                                                                                                                                                                              Armstrong, Nikaido, Marmelstein, Kubovcik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 256; DB 4; 31.1%; Pred. No. 5.8e-13;
                                                                                                                                                                                                                               US/08/383,682
                                                                            JP 2-230921
                                                                                                                                   2-167466
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; TYPE: PRT ; ORGANISM: cDNA clone US-10-085-476-2
                                                                                                                                                                                              CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 08/952,981
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PCT/IT96/00106
PRIOR FILING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: RM95A000343
PRIOR FILING DATE: 1995-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-085-476-2
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                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10085476 GENERAL INFORMATION:
Query Match
Best Local Similarity
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APPLICANT: Behrens, Sven-Brik
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
TITLE OF INVENTION: RNA-DEPENDENT RNA POLYMERASE AND TERMINAL NUCLEOTIDYL
TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/085,476
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: IT0002PCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: De Francesco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 440142
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     ENGTH: 2201
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 -AOVIAHOFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI-------
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Similarity 31.1%;
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Pred. No. 5.8e-13;
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14.1%;

Score 256; DB 26; Pred. No. 6.7e-13;

Length 2201;

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RESULT 15
US-07-769-996B-32
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                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-1

FILING DATE: 25-UN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-2

FILING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION UMMER: JP 2-3

FILING DATE: 09-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION UMMER: JP 2-3

FILING DATE: 09-NOV-1990

PRIOR APPLICATION DATA:
NFORMATION FOR SEQ ID NO:
                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 28-DEC-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Recurrent APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                REGISTRATION NUMBER: 31,404
REFERENCE/DOCKET NUMBER: 90
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: UFFILING DATE: 19911002 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER OF SEQUENCES:
                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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TAKAMIZAWA, Akahisa
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                                                    (202)
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                                                                                                                                                                                                               UMBER: JP 2-305605
09-NOV-1990
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31-AUG-1990
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MOLECULE TYPE:
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LENGTH: 2620 amino aci
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                                    QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                        -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
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Search completed: July 25, 2003, 13:19:47 Job time : 378 secs

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1: sp_archea:*
2: sp_bacteria:*
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sp_virus:*
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Q9QIX2
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Q9J3F8
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      RESULT 1
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     X MEDLINE=97335261; PubMed=9191927;
X MEDLINE=97335261; PubMed=9191927;
A Chamberlain R.W., Adams N., Saeed A.A., Simmonds P., Elliott R.M.;
A Chamberlain R.W., Adams N., Saeed A.A., Simmonds P., Elliott R.M.;
The predominant genotype in the Middle East.";
The predominant genotype in the Middle East.";
L. J. Gen. Virol. 78:1341-1347(1997).
C -:- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
C PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).

REMBL; Y11604; CAA72338.1; -.
REMBL; Y11604; CAA72338.1; -.
REMBL; Y11604; CAA72338.1; -.
REMBLSP; S29.001; -.
REMBROPS; S29.001; -.
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InterPro: IPR002531;
InterPro: IPR002518;
InterPro: IPR004109;
InterPro: IPR001745;
InterPro: IPR001745;
InterPro: IPR001868;
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O39929; PRELIMINARY; PRT; 3008 AA.
O1-9AN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
HCV polyprotein (Genome polyprotein).
Hepatitis C virus type 4a.
Wiruses; sernA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                    Hepacivirus.
NCBI_TaxID=31653;
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     InterPro;
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HCV_core.
HCV_env.
HCV_NS1.
HCV_NS3.
HCV_NS3.
HCV_NS4a.
HCV_NS4a.
HCV_NS4a.
HCV_NS5a.
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Q9Q1X2
Q9Q1X8
Q9Q1X7
Q9E1ES8
Q9D1ES
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Q9j3g6
Q9j3g6
Q9j3g6
Q9qiy9
P90qiy1
Q9ife5
Q9qiy1
Q9dix7
Q9dix8
Q9qix8
Q9qix8
Q9qix8
Q9qix8
Q9qix8
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Q81757
Q03463
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DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_env; 1.

DR Pfam; PF01560; HCV_NS1; 1.

DR Pfam; PF01560; HCV_NS2; 1.

DR Pfam; PF01506; HCV_NS2; 1.

DR Pfam; PF01001; HCV_NS4&; 1.

DR Pfam; PF01006; HCV_NS4&; 1.

DR Pfam; PF01006; HCV_NS4&; 1.

DR Pfam; PF01006; HCV_NS3&; 1.

DR Pfam; PF00198; Viral RdRP; 1.

DR Pfam; PF00198; Viral RdRP; 1.

DR Pfam; PF001998; Viral RdRP; 1.

DR Pfam; PF001908; Viral RdRP; 1.

DR PROSITE; PS00229; IG MHC; 1.

DR PROSITE; PS00229; IG MHC; 1.

DR PROSITE; PS00229; IG MHC; 1.

DR PROSITE; PS00521; RDRP_DOSITIVE; 1.

DR PROSITE; PS00521; RDRP_VIRAL; 1.

DR PROSITE; PS00507; RDRP_VIRAL; 1.

DR PROSITE; PS00
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Best Local
                                               Genome polyprotein.
Hepatitis C virus.
Viruses, ssrNA positive-strand
                                                                                                                                                                                                                                         STRAIN=MD29;
Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., "Characteristics of hepatitis C viral genome associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9J3G3;
01-OCT-2000
                             EMBL; AF207770; AAF65960.1; HSSP; P26663; 1JXP.
                                                                                                                                                                                                                                                                                                                                                                                          Hepacivirus.
NCBI_TaxID=11103;
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IPR007095; RNA_pol_DS_PS.
IPR007094; RNA_pol_PSvir.
  IPR000345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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CytC_heme_bind
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15,
23,
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Pred. No. 1
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l.7e-10;
les 72;
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disease
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RESULT
Q81825
ID Q8
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Best Local S
Matches 102
                                                                         Q81825 PRELIMINARY;
Q81825; CTEMBLE 1. 01, C
01-NOV-1996 (TEMBLE 1. 01, L
01-NOV-1996 (TEMBLE 1. 21, L
01-MAR-2003 (TEMBLE 1. 23, L
MRNA, complete cds (Genome po
Hepatitis C virus
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Pfam;
Pfam;
Pfam;
                                                     Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00190; CYTÓCHROME_C; 1.
PROSITE; PS50507; RDRP_POSITIVE; 1.
PROSITE; PS50521; RDRP_VIRAL; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane SEQUENCE 3010 AA; 327226 MW; 19783535650CACE3 CRC64;
  Hepacivirus.
NCBI_TaxID≈11103;
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Similarity 31.9%;
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5; IPR001490; HCV_NS4b.
5; IPR002868; HCV_NS5a.
6; IPR002166; HCV_RdRP.
7; IPR007095; RNA_Dol_DS_PS.
7; IPR007094; RNA_Dol_PSVir.
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HCV_core; 1
HCV_env; 1
HCV_env; 1
HCV_NS1; 1
HCV_NS2; 1
HCV_NS3; 1
HCV_NS3; 1
HCV_NS4b; 1
HCV_NS5a; 1
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HCV_NS1.
HCV_NS2.
HCV_NS3.
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HCV_core.
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                                                                                                             polyprotein)
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Pred. No. 1.7e-10;
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                                                                                                                                                                                                                                                        3010
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                                                     DNA stage; Flaviviridae;
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EDRONMIH

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Best Local S
Matches 102
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Pfam; PF01539; HCV_env; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01506; HCV_NS4a; 1.
Pfam; PF01506; HCV_NS4a; 1.
Pfam; PF01506; HCV_NS4a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prom; Pro1998; Viral RdRP; 1.

ProDom; PD186062; HCV_NS1; 1.

SWART; SW00467; DEXDC; 1.

PROSITE; PS50507; RDRP_POSITIVE; 1.

PROSITE; PS50507; RDRP_VORAL; 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane SEQUENCE 3010 AA; 326924 MW; FE997D54EE05142B CRC64;
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SEQUENCE FROM |
Cho J.-M.;
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InterPro;
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-- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLECCAPSID COVERED BY
-- LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
-- PROTEIN M AND GLYCOPROTEIN E. THE NUCLECAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002166; HCV_Ro
InterPro; IPR007095; RNA_po
InterPro; IPR007094; RNA_po
Pfam; PF01543; HCV_capsid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
102; Conserv
                                                                                                                 QFKEKVLAFASRGNHVSPRHYVPESEPQVVVT
                                                                                                                                                                     MPSAEDMVNLLPAILSPGALVVGIVCAAILRRHVGPGEGAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AAP-----VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIRSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQAQVI
                                                                                                                                                                                                                                                         GWVAAQLAPPSAASAFVGAGIAGAAVGTIGLGKVLVDILAGYGAGVAGALVAFK-IMSGE
                                                                                                                                                                                                                                                                                                 MMLAEQFKQKALAFASRGNHVAPTHYVTESDAK------PALVPDKEVLYQQ
                                                                                                                                                                                                                                                                                                                                                                                          AHQFKEKVLAFASRGNHDSPTHYVPESDAKPAIIPDREVLYREFDEMEESQH-LPYIEQG
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ilarity 30.7%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 268; DB 12;
Pred. No. 1.7e-10;
6; Mismatches 88
                                                                                                                                                                                                                                                                                                                                            -SITSPL---
                                                                                                                                                                                                                  -NHVAPTHYVVESDASASLPYMDETRAIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
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Best Local S
Matches 102
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Pfam; PF01543; HCV_capsid; 1.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01549; HCV_NS1; 1.

DR Pfam; PF01559; HCV_NS1; 1.

Pfam; PF01538; HCV_NS3; 1.

Pfam; PF01506; HCV_NS44; 1.

DR Pfam; PF01001; HCV_NS44; 1.

DR Pfam; PF01001; HCV_NS44; 1.

Pfam; PF01001; HCV_NS44; 1.

Pfam; PF01001; HCV_NS44; 1.

Pfam; PF01001; HCV_NS1; 1.

PR Pfam; PF01506; HCV_NS1; 1.

PR PF01508; HCV_NS1; 1.

PR PF01508; HCV_NS1; 1.

PR PF01508; HCV_NS1; 1.

PROSITE; PS50507; RDRP POSITIVE; 1.

PROSITE; PS50507; RDRP POSITIVE; 1.

PROSITE; PS50501; RDRP VIRAL; 1.

PROSITE; PS50521; RDRP VIRAL; 1.

PROSITE; PS50521; RDRP VIRAL; 1.

PROSITE; PS50521; RDRP POSITIVE; 1.

PROSITE; PS50521; RDRP POSITIVE
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Q68285;
Q68285;
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SEQUENCE FROM N.A.
Cho J., Park Y., Lee Y., Yang J.,
Cho J., Park Cloning of Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS.
- PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand Hepacivirus.
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Hepatitis C virus.
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01-NOV-1996 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ); IPR001410; DEAD.

); IPR002522; HCV_capsid.

); IPR002521; HCV_core.

); IPR002511; HCV_NS1.

); IPR002511; HCV_NS2.

); IPR001409; HCV_NS3.

); IPR001490; HCV_NS4a.

0; IPR001490; HCV_NS4b.

0; IPR00166; HCV_RGA.

0; IPR00166; HCV_RGA.

0; IPR00166; HCV_RGA.

0; IPR001094; RNA_Dol_DS_PS.

0; IPR007094; RNA_Dol_DS_PS.

0; IPR007094; RNA_Dol_DS_PS.
GWVÄAQLAPPSAASÁFVGAGIAGAAVGTIGLGKVLVDILAGYGAGVAGÁLVAFK-IMSGE 1872
                                                                                                                                                                                                                                                                                 KPAIIPDREVLYQEFDEMEECASHLPYFEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                                                                                                                                                                                                                                                                                              RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
                                                                                                                                                                                                                                  VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQAQVI
                                            MMLAEQFKQKALAFASRGNHVAPTHYVTESDAK--
                                                                                                                             AHQFKEKVLAFASRGNHDSPTHYVPESDAKPAIIPDREVLYREFDEMEESQH-LPYIEQG
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                                                                                                                                                                                      -VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIRSP---
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                   Score 268;
Pred. No. 1
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.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                               88;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3010;
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                                            PALVPDKEVLYQQ
                                                                                           -TTQHTLLFNILG
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                                                                           Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01560; HCV_NS2; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4s; 1.
Pfam; PF01906; HCV_NS4s; 1.
Pfam; PF00998; Viral RdRP; 1.
Pfam; PF00998; Viral RdRP; 1.
PF0000m; PD186602; HCV_NS1; 1.
Pfam; PF00998; Viral RdRP; 1.

ProDom; PD186062; HCV NS1; 1.

SMART; SMO0487; DEXDC; 1.

PROSITE; PS50507; RDRP_POSITIVE; 1.

PROSITE; PS50521; RDRP_VIRAL; 1.

Coat protein; Envelope_protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transferase; TransEQUENCE 3010 AA; 326902 MW; 04233B5981E71EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome polyprotein.
Hepatitic C virus.
Viruses; ssRNA positive-strand
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InterPro;
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Sakamoto N.,
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01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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01-MAY-2000
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Tazawa J.i., Izumi N., Marumo F., Sato
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                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 263:244-253(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Time-related changes in full-length hepatitis
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SUBUNIT: THE VIRI
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                                                                                                                                                                                           IPR002521; HCV_core.
IPR002521; HCV_core.
IPR002519; HCV_env.
IPR002531; HCV_NS1.
IPR002531; HCV_NS3.
IPR000740; HCV_NS3.
IPR0007496; HCV_NS4A.
IPR0001490; HCV_NS4A.
IPR0021668; HCV_NS4A.
PR0021668; HCV_RSA.
PR002166; HCV_RSA.
PR007095; RNA_PO1_DS_PS.
PR0070994; RNA_PO1_DS_PS.
PR0070994; RNA_PO1_DS_PS.
PR0070994; RNA_PO1_PSVir.
3; HCV_core; 1
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                                                                                                                                                                                                                                                                                                                                          IPR002519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurosaki M., Enomoto N., Maekawa S., Miyasaka Y.,
Fukuma T., Tazawa J., Izumi N., Marumo F., Sato C.;
UL-1999) to the EMBL/GenBank/DDBJ databases.
THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viruses,
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O C.;
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                                                                                     Q68949;
Q68949;
01-NOV-1996
  Pfam;
Pfam;
Pfam;
Pfam;
                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                          Gene
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=93013055; PubMed=1327977;
                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                    JK1-full protein
                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-MAR-2003
                                          InterPro; IPRO
Pfam; PF01543;
                                                                                                                                                                                                                                                                  Honda M., Kaneko S., Unoura U., Kobayashi K., "Sequence comparisons for a hepatitis C virus a patient with liver cirrhosis.";
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11103;
                                                                InterPro;
                                                                         InterPro;
                                                                                                                             interPro;
                                                                                                                                        interPro;
                                                                                     nterPro;
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                                                                                                                   nterPro;
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                                                                                                                                                            nterPro;
                                                                                                         nterPro;
                                                                                                                                                                                                             SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS PROTEIN AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).
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                       PF01539;
                                                                                                                                                                                                     X61596; CAA43793.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AEAAVP---VVESKWQALEAFWAKHMWNFISGIQYLAGLSTLPGNPAI-----
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                                                                                                                            IPR002531;
IPR002518;
                                                                                               IPR001490;
                                                                                                                   IPR004109;
                                                                                                                                                  IPR002519;
                                                                                                                                                             IPR002521;
                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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HCV_capsid;
HCV_core; 1;
HCV_env; 1.;
HCV_NS1; 1.;
HCV_NS2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ASLMÁFTASVTSPLTTOYT--
                                                                         HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS5a.
HCV_RdRP.
                                                                                                                                                   HCV_core.
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29.7%;
                                                     RNA_pol
                                                                                                                                                                                                                                                                                                                                                                                     polyprotein)
                                                                                                                                                                       capsid
                                          ol_DS_PS.
ol_PSvir.
1.
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Pred. No. 3.9e.
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                      viruses,
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.9e-10;
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genome RN
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Best Local S
Matches 87
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Pfam; PF01006; HCV NS4a; 1.
Pfam; PF01001; HCV NS4b; 1.
Pfam; PF01506; HCV NS5a; 1.
Pfam; PF005098; Viral RdRP; 1.
ProDom; PD186062; HCV NS1; 1.
SMART; SM00487; DEXDC; 1.
EMBL;
HSSP;
                                         "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                            Genome polyprotein. Hepatitis C virus.
                                                                                                                                                                            01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
CHAIN
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CHAIN
                                                                                                                                              Hepatitis C virus.
Viruses, ssRNA positive-strand
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                                                                                      Takahashi K., Iwat
Hatahara T., Ohta
                                                                                                                               NCBI_TaxID=11103;
                                                                                                                                                                                                       Q9DTE2;
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                                                                               Mishiro S.;
                                                                                                         STRAIN=HCVT169;
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                                                                                                                SEQUENCE FROM N.A.
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               LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA (BY SIMILARITY).
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384
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1007
1616
1863
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3010
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                                                                                    Iwata K.,
Ohta Y.,
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1615
1862
2013
                                                                                     K., Matsumoto M., Matsumoto H., Nakao K., Kanai K., Maruo H., Baba K., Hijikata
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NON-STRUCTURAL 2.

NON-STRUCTURAL 3.

NON-STRUCTURAL 4A.

NON-STRUCTURAL 4B.
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Pred. No. 3.
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W; 451740D8FF6134DA CRC64;
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annotation updat
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                                                                                                                                                   DNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
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                                                                                  , Nakao K.,
                                                                                                                                                   Flaviviridae;
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Best Local S
Matches 86
                                      Genome polyprotein.
Hepatitis C virus.
Viruses; ssRNA positive-strand
                                                                  01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                              Q9J3H9
Q9J3H9;
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Pfam;
                      Hepacivirus.
NCBI_TaxID=11103;
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Pfam;
SEQUENCE FROM N.A STRAIN=MD13;
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Pfam;
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                                                                                                       PRELIMINARY;
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ProDom; PD186062; HCV NS1, 1.
SMART; SM00487; DEXDC; 1.
PROSITE: PROPERTY P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00190; CYTOCHROME C; 1.
PROSITE; PS50507; RDRP POSITIVE; 1.
PROSITE; PS50521; RDRP_VIRAL; 1.
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5; IPR001490; HCV_NS4b.
5; IPR002868; HCV_NS5a.
5; IPR002166; HCV_RGRP.
6; IPR007095; RNA_pol_DS_PS.
6; IPR007094; RNA_pol_PSvir.
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VQWMNRLIAFASRGNHVSPTHYVPESDA 1940
                                              EQFKQKALAFASRGNHVAPTHYVTESDA
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                                                                                                                                                                                           AGYGAGVAGALVAFKVMSGDMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA
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HCV_env; 1.
HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS4a; 1.
HCV_NS4a; 1.
HCV_NS5a; 1.
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                                                                                                                                                                                                                                                                                    -IPDREVLYREFDEMEESQHL--PYIEQGMML--
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red. No. 5.5e-10;
Mismatches 74;
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Best Local
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InterPro; IPR002531; HCV NS1.
InterPro; IPR002518; HCV NS2.
InterPro; IPR004109; HCV-NS3.
InterPro; IPR004109; HCV-NS4a.
InterPro; IPR0001499; HCV-NS5a.
InterPro; IPR002868; HCV-NS5a.
InterPro; IPR002166; HCV RdRP.
InterPro; IPR007094; RNA_pol_DS FInterPro; IPR007094; RNA_pol_DS FInterPro; IPR007094; RNA_pol_PSVi
Pfam; PF01543; HCV-core; 1.
Pfam; PF01543; HCV-env; 1.
Pfam; PF01539; HCV-env; 1.
Pfam; PF01539; HCV-NS1; 1.
Pfam; PF01539; HCV-NS1; 1.
Pfam; PF01538; HCV-NS2; 1.
Pfam; PF01538; HCV-NS3; 1.
Pfam; PF01536; HCV-NS3; 1.
Pfam; PF01006; HCV-NS4a; 1.
Pfam; PF01006; HCV-NS4a; 1.
Pfam; PF01006; HCV-NS4a; 1.
Pfam; PF01006; HCV-NS5a; 1.
Pfam; PF010998; Vital RdRP; 1.
Q9QIX2
Q9QIX2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD186062; HCV NS1; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS00100
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PROSITE; PS00507; RDRP_POSITIVE; 1.
PROSITE; PS50521; RDRP_VIRAL; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 326984 MW; AF12CC00E0A8B078 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   progression.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
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HSSP; P26663; 10
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"Characteristics
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                                                                                                                               QWMNRLIAFASRGNHVSPTHYVPESDA
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                                                                                                                                                                                                                                          -----PYIEQGMML--
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IPR002519;
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IPR001410; DEAD.
 (TrEMBLrel 13,
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 5.5e
27; Mismatches
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disease
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Best Local
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-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).

EMBL; AF165063; AAD56198.1; -.
                                                                                                                                                                                                                                                                        Coat protein; Envelope protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transferase; Trans SEQUENCE 3010 AA; 326855 MW; 3806A4AF819ED552 CRC64;
                                                                                                                                                                                                                                                                                                                               PROSITE; PS50507; RDRP_POSITIVE; 1.
PROSITE; PS50521; RDRP_VIRAL; 1.
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NCBI_TaxID=11103;
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Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 263:244-253(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagayama K., Kurosaki M., Enomoto N., N
Tazawa J.i., Izumi N., Marumo F., Sato
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n; PF01542; HCV_core; 1.
n; PF01539; HCV_cnv; 1.
n; PF01560; HCV_NS1; 1.
n; PF01538; HCV_NS2; 1.
n; PF01006; HCV_NS3; 1.
n; PF01006; HCV_NS4b; 1.
n; PF01006; HCV_NS4b; 1.
n; PF01006; HCV_NS5a; 1.
n; PF01006; HCV_NS5a; 1.
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| IPRO04109
| IPRO04109
| IPRO07459
| IPRO02868
| IPRO02868
| IPRO02868
| IPRO07095
                                                                                                                         RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
           IAHQFKEKVLAFASRGNHDSPTHYVPESDAKPAIIPDREVLYREFDEMEESQHLPYIEQG
                                                  ----AAPVVESKWOAL------EAFWAKHMWNFISGIOYLAGLSTLPGNPAI----
                                                                                    VPESDARPAIIPDREVLHREFDEMEEAFASR--GNHVSPAHYVPESDASQAAPYIEQAQV
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IPR002521;
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                                                                                                                                                                                                                     261;
No. 5
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                        Pfam; PF00998; Viral RdRP; 1.
ProDom; PD186062; HCV NS1; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS50507; RDRP POSITIVE; 1.
PROSITE; PS50521; RDRP_VIRAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
Pfam;
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InterPro;
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01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trowbridge R., Gowans E.J.;
"Molecular cloning of an Australian isolate of hepatitis C virus.",
Arch. Virol. 143:501-511(1998).
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome polyprotein.
Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trowbridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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P26663; 1J
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PF01560;
PF01538;
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PF01542;
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                                                                                                                                                                           HCV_NS4a; 1.
HCV_NS4b; 1.
HCV_NS5a; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     _capsid;
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HCV_core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4b.
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HCV_RdRP.
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protein; Glycoprotein; Nonstructural
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protein;
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Best Local
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InterPro;
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   InterPro;
                                                           nterPro;
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                     IPRO00345; CytC_heme_bind.
IPRO01410; DEAD.
IPRO02522; HCV_capsid.
IPRO02521; HCV_core.
IPRO02521; HCV_env.
IPRO02531; HCV_env.
IPRO02531; HCV_NS3.
IPRO02531; HCV_NS3.
IPRO04109; HCV_NS3.
IPRO04109; HCV_NS44.
                                                                                          IPR00251
                                                                                                                      IPR002531;
                                                                                                                                                                                                             IPR002522;
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progression.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID
                                                                                                                                                                                  Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                     SEQUENCE FROM N.A. STRAIN=MD25;
                                                                                                                                                                                                                     Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                   Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein;
CHAIN
                                                                                              Nagayama K., Kurosaki M., Enomoto N., Characteristics of hepatitis C viral
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                           QWMNRLIAFASRGNHVSPTHYVPESDA 1940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DASQAAPYIEQAQVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPAIIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AEAAVP---VVESKWQALEAFWAKHMWNFISGIQYLAGLSTLPGNLAIASLMAF 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        810
1027
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                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                 Kurosaki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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1026
1657
1711
1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NS4A PROTEIN.
NS4B PROTEIN.
NS5A PROTEIN.
NS5B PROTEIN.
NS5B PROTEIN.
NS5B PROTEIN.
                                                                                                                                                                                                                                                                                                         Created)
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Last annotation updat
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NS2 PROTEIN.
NS3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E1 PROTEIN.
E2 PROTEIN.
P7 PROTEIN.
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Pred. No. 6.4e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase;
CORE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AHQFKEKVLAFASRGNHDSPTHYVPESD 165
                                                                                                                                                                                                                     viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                         3010
                                                                                                  Miyasaka Y., Marun
genome associated
                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                        update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                 TWO PROTEINS IS A COMPLEX
                                                                                                   Marumo F., iated with
                                                    COVERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                   , Sato C.;
disease
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                                                  ВУ
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HCV_NS4b

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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002868; HCV_NS5a.

R InterPro; IPR00156; HCV_RdRP.

RR InterPro; IPR001650; Helicase C.

R InterPro; IPR007095; RNA pol DS PS.

R InterPro; IPR007094; RNA pol DS PS.

R InterPro; IPR007094; RNA pol DS PS.

R Pfam; PF01543; HCV_Capsid; 1.

R Pfam; PF01539; HCV_NS2; 1.

R Pfam; PF01539; HCV_NS2; 1.

R Pfam; PF01539; HCV_NS3; 1.

R Pfam; PF01006; HCV_NS3; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF01006; HCV_NS4a; 1.

R Pfam; PF01071; Hclicase C; 1.

R Pfam; PF00271; hclicase C; 1.

R Pfam; PF00998; Viral_RdRP; 1.

R Pfam; PF018062; HCV_NS1; 1.

R Pfam; PF01970; DEXDC; 1.

R PROSITE; PS00190; CYTOCHROME_C; 1.

PROSITE; PS00190; CAPCP_VIRAL; 1.

ATP-binding; Coat protein; Envelope protein; Glycoprotein; Hellydrolase. Nonstructural protein; Dolumroffin.
                                                                                                                                                                                                                                                                   Q9DTE5 PRELIMINARY;
Q9DTE5;
Q9DTE5;
Q1-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2003 (TrEMBLrel. 23, L
01-MAR-2003 (TrEMBLrel. 23, L
Genome polyprotein.
Hepatitis C virus.
"Heparitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-i- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
                                                                                                                                                  STRAIN=HCVT145;
                                                                                                      Takahashi K., Iwata K., Matsumoto M.,
Hatahara T., Ohta Y., Kanai K., Maruo
                                                                                                                            Takahashi K.,
                                                                                                                                                                                                          Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane SEQUENCE 3010 AA; 326507 MW; 9EEAC8ADA4B441DF CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 -- AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOWMNRLIAFASKGNHVSPTHYVPESDA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPESDARPAIIPDREVLHREFDEMEEAFASR--GNHVSPAHYVPESDASQAAPYIEQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPAVVPDREVLYREFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTASKQAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTASITSPLTTQSTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AAPVVESKWRAL-----EAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMA 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
ilarity 32.1%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 260; DB 12;
Pred. No. 6.4e-10;
27; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                      viruses,
                                                                                                                                                                                                                                                                                                                                                                                                        3010
                                                                                                      Matsumoto H., H., Baba K.,
                                                                                                                                                                                                                                                        no
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                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                      stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                      , Nakao K.,
Hijikata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80;
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  RESULT 13
Q9J3F4
ID Q9J3F
AC Q9J3F
DT 01-OC
DT 01-OC
DT 01-MA
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Best Local S
Matches 85
Q9J3F4
Q9J3F4;
01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00190; CYTOCHROME C; 2.

PROSITE; PS50507; RDRP_POSITIVE; 1.

PROSITE; PS50507; RDRP_VIRAL; 1.

ATP-binding; Coat protein; Envelope protein; Glycoprotein;
ATP-binding; Coat protein; Envelope protein;
Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 326986 MW; 573C0F3C55B3F3F4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro;
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                                                                                                                                                                                           1914
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                                                                                                                                                                                                                                202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00271;
PF00998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01539;
PF01560;
PF01538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P27958; 1HEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 RPĀVIPDREVLYQEFDEMEE-ĀSHLPYIEQGMQLĀEQFKQKĀLĀF---ĀSRQNHVSPTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00271; helīcase C; 1.
PF00998; Viral RdRP; 1.
; PD186062; HCV_NS1; 1.
SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPAVVPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA----
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IPRO02521;
IPRO02531;
IPRO02531;
IPRO045109;
IPRO04109;
IPRO01490;
IPRO01490;
IPRO02166;
IPRO01650;
                                                                                                                                                                                         QWMNRLIAFASRGNHVSPTHYVPESDA
                                                                                                                                                                                                                   QFKQKALAFASRGNHVAPTHYVTESDA
                                                                                                                                                                                                                                                                            GYGAGVAGALVAFKVMSGEMPSTEDMVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV
                                                                                                                                                                                                                                                                                                                 -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                                                                                                                                                                                                                           TASITSPLTTQNTLMFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA
                                                                                                                                                                                                                                                                                                                                                                                                    -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AAP-----VVESKWRALEGFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000345;
IPR001410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR007094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR007095;
  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV_capsid;
HCV_core; 1.
HCV_env; 1.
HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS3; 1.
HCV_NS4; 1.
HCV_NS4b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENVELOPE. THE ENVELOPE CONSISTS OF ND GLYCOPROTEIN E. THE NUCLEOCAPSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAB18805.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4b.
HCV_NS4b.
HCV_NS5a.
HCV_RdRp.
HCV_RdRp.
HCV_RdRp.
HCV_RDI_DS_PS.
RNA_pol_DS_PS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CytC_heme_bind
  15,
15,
23,
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Last sequence update)
Last annotation update)
                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 260; DB 12;
Pred. No. 6.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                     3008
                                                                                                                                                                                                                                228
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IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicase;
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                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO F PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                 ATP-binding; Coat protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane. SEQUENCE 3008 AA; 326834 MW; 99AE09E14C3109F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00190; CYTOCHROME C; 1. PROSITE; PS50507; RDRP_POSITIVE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              progression."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marun "Characteristics of hepatitis C viral genome associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MD34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50521; RDRP_VIRAL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                               PF00271; helicase C; 1.
PF00998; Viral RdRP; 1.
m; PD186062; HCV_NS1; 1.
; SM00487; DEXDC; 1.
                                                                                                                                                   79
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                                                                                                                                                                                                                                                   l Similarity
86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyprotein
                                                                                                                                                                                                    RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
                                                                                                                                                VPESDARPAIIPDREVLHREFDEMEEAFASR--GNHVSPAHYVPESDASQAAPYIEQ---
                                              FTASITSPLTTQSTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDIL 1850
                                                                               --AQVIAHQFKEKVLAF-----
                                                                                                                                                                                 KPAVIPDREVLYREFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR000345; CytC_heme_bind
                                                                                                                                                                                                                                                   Conservative
                                                                                                                  -AAPVVESKWRAL---
             ---IPDREVLYREFDEMESSOHL--PYIEQGMML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV_capsid.
HCV_core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA_pol
                                                                                                                                                                                                                                                                  14.2%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV_NS4a.
HCV_NS4b.
HCV_NS5a.
HCV_RdRP.
                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                               Score 259; DB 12;
Pred. No. 7.6e-10;
""matches 74;
                                                                                 ASRGNHDSPTHYVPESDAKPAI ------
                                                                                                                  EAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMA 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                              Length 3008;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWO PROTEINS:
IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marumo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mo F.,
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                                                                                                                                                                                                                                                   80;
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disease
                                                                                                                                                                                                                                                   Gaps
                 200
                                                                                 170
                                                                                                                                                   133
                                                                                                                                                                                  1743
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                                                                                                                                                                                                                                                   10;
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Q68788
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                                                                                                               Ouery Match
Best Local
                                                                                                                                                        PROSITE; PS50507; RDRP POSITIVE; 1.
PROSITE; PS50507; RDRP VIRAL; 1.
Coat protein; Envelope protein; Glycopelyprotein; RNA-directed RNA polymera SEQUENCE 3010 AA: 322000
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seki M., Honda Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV polyprotein (Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q68788
                                                                                                                                                                                                                                                                                    Pfam; PF00998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               068788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibiting Hepatitis C virus gene expression:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterPro;
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                                 1691
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D45172; BAA08120.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P26663; 1JXP
 79
                                                                                                                  Similarity
                                                                                                                                                                                                                                                           00998; Viral RdRP; 1.
PD186062; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                    RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQAQVI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR004109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR00251
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  HCV_capsid;
HCV_core; 1
HCV_env; 1:
HCV_NS1; 1:
HCV_NS2; 1:
HCV_NS3; 1:
                                                                                                                                                                                                                                                                                                   HCV_NS4b; 1.
HCV_NS5a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8720135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV_core.
                                                                                                                14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capsid
                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     l_DS_PS.
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                                                                                                                  Score
Pred.
                                                                                                                                                                                 polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                  Glycoprotein; Nonstructural olymerase; Transferase; Trans
                                                                                                   Mismatches
                                                                                                                                                                     EED840E6A050E766 CRC64;
                                                                                                                  259; DB 12;
No. 7.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ņo
                                                                                                   109;
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Length 3010;

Transmembrane

protein;

Indels

; 98

Gaps

1745 78 11;

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J. Biochem. 118:1199-1204(1995).

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MENA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA 1910
                                                                                                                                                                                                                    antisense oligodeoxynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA stage; Flaviviridae;
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                                                                                                                                                                                           vitro
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  Interpro; IPR007522; HCV_capsid.
Interpro; IPR007521; HCV_capsid.
Interpro; IPR007521; HCV_core.
Interpro; IPR007531; HCV_NS1.
Interpro; IPR007531; HCV_NS1.
Interpro; IPR007531; HCV_NS2.
Interpro; IPR00745; HCV_NS3.
Interpro; IPR00745; HCV_NS4a.
Interpro; IPR00745; HCV_NS4a.
Interpro; IPR00746; HCV_NS5a.
Interpro; IPR00746; HCV_NS5a.
Interpro; IPR00746; HCV_NS5a.
Interpro; IPR00795; RNA_pol_DS_PS_INTERPO; IPR007095; RNA_pol_DS_PS_INTERPO; IPR007094; RNA_pol_PS_INTERPO; IPR007094; RNA_pol_PS_INTERPO; IPR007094; RNA_pol_PS_INTERPO; IPR007094; RNA_pol_PS_INTERPO; IPR007095; RNA_pol_PS_INTERPO; IPR007094; RNA_pol_PS_INTERPO; IPR007095; RNA_pol_PS_INTERPO; IPR007094; RNA_pol_PS_INTERPO; IPR007095; INTERPO; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9QIX3 PRELIMINARY;
Q9QIX3;
01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 23, L.
01-MAR-2003 (TrEMBLrel. 23, L.
Genome polyprotein.
Hepatitis C virus.
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7LT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF165062; AA
HSSP; P26663; 1NS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nagayama K., Kurosaki M., Enomoto N., Maekawa S., Miyasaka Y., Sakamoto N., Fukuma T., Tazawa J., Izumi N., Marumo F., Sato C.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases -:- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20013325; PubMed=10544098;
Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka Y., Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MD9-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MD9-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 263:244-253(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepacivirus.
NCBI_TaxID=11103;
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Last annotation update)
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Best Local
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Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; Viral RdRP; 1.
ProDom; PD186062; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
Coat protein; RSRP_VIRAL; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; POlyprotein; RNA-directed RNA polymerase; Transferase; Transmembrane.
SEQUENCE 3010 AA; 327253 MW; 9F1B0B3F536774FA CRC64;
     1914
                                                                                                                                                                                                                                                           1691 RPAVIPDREVLYREFDEMEBCASHLPYIEQGMQLAEQFKQKALGLLQTATKQ------
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GYGAGVAGALVAFKIMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                                                                                                                       VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                          TASITSPLTTONTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA 1853
                                                                                                                                                           -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI-----
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                                                                                               -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
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Pred. No. 7.6e-10;
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1818
1 AAHIPYLEQGMHLAEQFKQK......KAALIEEGQRMAEMLKSKIQ 352
                                                                                                                                                                                                                                                                                                                                                                                             July 25, 2003, 12:55:06 ; Search time 23 Seconds (without alignments) 719.713 Million cell updates/sec
                                                                                                                                                                                                                127863 segs, 47026705 residues
SwissProt_41:*
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Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	BB	ID	
	260	14.3	3010	-	POLG_HCVJA	666
2	258		3010	ب	POLG_HCVTW	29846 h genome
w	256		2	<u>س</u>	POLG_HCVBK	6663 h genome
.4.	256	4	2	-	POLG_HCVJT	0269 h
رب ر	254	14.0	3011	ب	POLG_HCV1	664 h genome
6	247	13.	3011	س	POLG_HCVH	7958 h genome
7	203.5	_	2	μ	POLG_HCVJ6	h genome
8	201.5	11.	3	μ	POLG_HCVJ8	6661 h genome
9	121.5		911	,	AAC4_RAT	qxq0 rattus no
10	120.5		5327	۳	MACF_MOUSE	0
11	114.5		912	۲	AAC4_MOUSE	P57780 mus musculu
12	114.5	<u>ه</u>	4473	۲	PLE1_CRIGR	5 crice
13	113.5	6.	911	۳	AAC4_HUMAN	707 homo
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16	107.5	<u>ښ</u>	1733	Ъ	RPB1_YEAST	0
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18	106.5	<u>ن</u>	1736	ب	-11	7
19	106		2748	1	NUM1_YEAST	N
20	104	•	964	μ	IF3A_YEAST	ø
21	103	5.7	3259	μ	GIAN_HUMAN	Q14789 homo sapien
22	103	·	5430	μ	MACF_HUMAN	3 homo
23	103	•	5938	۳	MAC4_HUMAN	homo
24	101.5	·	788	سر	PCAP HUMAN	homo
25	101.5		2517	۲	NCR2_HUMAN	h nuc
26	101	·	478	۲	ATPB_AQUAE	ag
27	101		1036	Ц	DP3A_STRP8	55.5
28	101	·	67	ب	DMD MOUSE	_
29	100		478	Ь	ATPB_AQUPY	92 agui
30	100		649	,,,	DREB HUMAN	•
31	100	5.5	1036	۳	DP3A_STRP3	-
32	100		1036	ب	DP3A_STRPY	9
33	100	5.5	1745	ب	ZO1_MOUSE	7 mu

45	44	43	42	41	40	39	38	37	36	35	34
96	96	96.5	96.5	97	97	97	97.5	97.5	98.5	98.5	99
5.3	5.3	5	5 . 3	5.3	ა	5.3	5.4	5.4	5.4	5.4	5.4
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ALIGNMENTS

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his SWISS-PROT entry is copyright. It is produced through a collaborati etween the Swiss Institute of Bioinformatics and the EMBL outstation he European Bioinformatics Institute. There are no restrictions on is by non-profit institutions as long as its content is in no would do not this statement is not removed. Usage by and for commercinities requires a license agreement (See http://www.isb-sib.ch/announcresend an email to license@isb-sib.ch).	NUMA NIGHCUJA STANDARD; PRT; 3010 AA. 26662; 1-AUG-1992 (Rel. 23, Created) FEBE-2003 (Rel. 41, Last sequence update) FEBE-2003 (Rel. 41, Last annotation update) FOR Dipprotein [Contains: Capsid protein C (Core protence polyprotein [Contains: Capsid protein C (Core protence polyprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP32) (GP35); Envelope glycoprotein E2 (GP32) (GP35); Envelope glycoprotein MSG (GP36); Nonstructural protein MSG (GP37); Nonstructural protein MSG (GP37); Nonstructural protein MSG (GP37); Nonstructural protein MSG (P70) (Hepacivirin) (GP36); Nonstructural protein MSGA (P4); Nonstructural protein MSGA (P56); Nonstructural	7LT 1

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INTERPRO; IPROUZ52; HCV____
InterPro; IPRO02521; HCV____
InterPro; IPRO02521; HCV_core
InterPro; IPRO02519; HCV_env.
InterPro; IPR002511; HCV_NS1.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002161; HCV_NS4.
InterPro; IPR001409; HCV_NS48.
InterPro; IPR001490; HCV_NS48.
InterPro; IPR002166; HCV_NS58.

ThterPro; IPR002166; HCV_RdRP.
ThterPro; IPR001650; Helicase C.
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                Query Match
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Pfam; PF01508; HCV_NS1; 1.
Pfam; PF01538; HCY_NS2; 1.
Pfam; PF01508; HCY_NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF001506; HCV_NS5a; 1.
Pfam; PF00998; Viral_RdRP; 1.
Pfam; PF00998; Viral_RdRP; 1.
ProDom; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDc; 1.
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InterPro; IPR007094;
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Pro; IPR007094; RNA pol
PF01543; HCV_capsid; 1.
PF01542; HCV_core; 1.
 Similarity
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CAPSID PROTEIN C (POTENTIAL).

MAIRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein E2 (GF68) (GP70) (NSI); Protein P7; Nonstructural protein NS2 (P21) (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS5B (P50); Nonstructural Revolution NS5B (P50) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
NS5B (P50) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate Taiwan) (HCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
                                                                                                                                                                                                                                                         RNA (N).

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS. PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLG_HCVTW
P29846;
            EMBL; M84754; -; NOT_ANNOTATED_CDS
PIR; A40244; GNWVTW.
                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virology 188:102-113(1992).
-!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92230206; PubMed=1314449; Chen P.J., Lin M.H., Tai K.F., Liu P.C., Lin C.J., Chen D.S.; "The Taiwanese hepatitis C virus genome: sequence determination mapping the 5' termini of viral genomic and antigenomic RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCVTW
                                                                                                                                                                                                                                   -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepacivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=31645;
                                                                                                                                                                                                                                                                                                                                                  HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viprecursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                   LIPOPROTEIN ENVELOPE. THE EPROTEIN MAND GLYCOPROTEIN PROTEIN C AND MRNA.
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PF01001;
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PF01539;
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PF02907;
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1PR001410; DEAD:
1PR002522; HCV capsid.
1PR002521; HCV core.
1PR002513; HCV ws.
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1PR002518; HCV ws.
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1PR004109; HCV ws.
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1PR001490; HCV ws.
1PR002166; HCV ws.
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19; HCV env; 1

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HCV NS4b; 1

HCV NS5a; 1
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MAJOR ENVELODE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NS1/EZ (POTENTIAL).
NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
PROTEASE/HELICASE NS3 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
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Matches 85
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01-AUG-1992 (Rel.:
01-AUG-1992 (Rel.:
15-SEP-2003 (Rel.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (CP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.21.9); Protease/helicase NS3 (P70) (Hepacivirin) (EC 3.4.21.98); Nonstructural protein NS48 (P4); Nonstructural protein NS48 (P27); Nonstructural protein NS48 (P56); Nonstructural protein NS48 (P56); Nonstructural protein NS58 (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate BK) (HCV).
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X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1027-1210 AND 1678-1691. MEDLINE=98227846; PubMed=9568891; Yan Y., Li Y., Munshi S., Sardana V., Cole J.L., Sardana M., Steinkuehler C., Tomei L., de Francesco R., Kuo L.C., Chen Z.; "Complex of NS3 protease and NS4A peptide of BK strain hepatitis virus: a 2.2-A resolution structure in a hexagonal crystal form."
                                                                                                                          Love R.A., Parge H.E., Wickersham J.A., Hostomsk Moomaw E.W., Adachi T., Hostomska Z.; "The crystal structure of hepatitis C virus NS3 trypsin-like fold and a structural zinc binding
                                                                                                                                                                                                                                      MEDLINE=96235224; PubMed=8647104;
Borowski P., Heiland M., Oehlmann K., Becker B., Kornet.
"Non-structural protein 3 of hepatitis C virus inhibits
phosphorylation mediated by cAMP-dependent protein kinal
phosphorylation for the protein kinal
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                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1487-1500
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NCBI_TaxID=11105;
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NE=97015088; PubMed=8861916;
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DR PDB; 1JXP; 14-JAN-98.

PDB; 1JXP; 14-JAN-98.

PDB; 1CSJ; 06-NOV-99.

PDB; 1CSJ; 06-NOV-99.

PDB; 1CSJ; 06-NOV-99.

PDB; 1CSJ; 06-NOV-99.

PDB; 1CSJ; 09-APR-02.

PDB; 1CSJ; 1CPR001410; DEAD.

DR InterPro; IPR002521; HCV_capsid.

DR InterPro; IPR002519; HCV_NS3.

DR InterPro; IPR002519; HCV_NS4A.

InterPro; IPR002519; HCV_NS4A.

InterPro; IPR002166; HCV_NS4A.

InterPro; IPR002166; HCV_NS4A.

DR InterPro; IPR002166; HCV_NS4A.

DR InterPro; IPR002166; HCV_NS2; 1.

Pfam; PP01542; HCV_capsid; 1.

Pfam; PP01542; HCV_capsid; 1.

DR Pfam; PP01542; HCV_NS2; 1.

Pfam; PP01542; HCV_NS2; 1.

DR Pfam; PP01543; HCV_NS3; 1.

Pfam; PP01543; HCV_NS3; 1.

Pfam; PP01541; HCV_NS3; 1.

DR Pfam; PP01006; 
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C: -! FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE C: -! PROPROHEIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

C: -CATALTTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral procursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1.

C: -CATALTTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + C (ANA)(N).

C: -CATALTTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + C (ANA)(N).

C: -I SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN C AND MRNA.

C: -I SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY $29.
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A38465; GNWVTC.
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CAPSID PROTEIN C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS.1/E2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).
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Conservative 31; Mismatches
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MEDLINE=92295714; PubMed=1318627; Tanaka T., Kato N., Nakagawa M., Ootsuyama Y., Cho M.J., Tanaka T., Hijikata M., Ishimura Y., Shimotohno K.; Nakazawa T., Hijikata M., Ishimura Y., Shimotohno K.; Nakazawa T., Hijikata M., Ishimura Y., Shimotohno K.; William C. Virus genome from a single Japanese carrier: sequence variation within the same individual and among infected individuals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Genome polyprotein (Contains: Capsid protein C (Core protein (P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS4B (P27); Nonstructural protein NS4B (P27); Nonstructural protein NS5B (P30) (P70) (RNA-directed RNA pollymerase) (EC 2.7.7.48)].
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                    EMBL; D11168; BAA01943.1; -. PIR; A45573; A45573.
                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.

PROTEIN C AND MRNA.

THE DECEMBER OF PELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                             US Res. 23:39-53(1992).

FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the v precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
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                                                                                                                SEQUENCE
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Pfam; PF00998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); IPR002518; HCV_NS2.
); IPR0004109; HCV_NS3.
); IPR000745; HCV_NS4a.
); IPR001490; HCV_NS4b.
); IPR0012868; HCV_NS5a.
); IPR002166; HCV_NS5a.
); IPR007095; RNA_PO1_DS_PS.
); IPR007094; RNA_PO1_PSVir.
P01542; HCV_core; 1.
P01542; HCV_env; 1.
P01539; HCV_env; 1.
P01539; HCV_NS1; 1.
P01539; HCV_NS1; 1.
P01539; HCV_NS1; 1.
P01539; HCV_NS2; 1.
P01539; HCV_NS4b; 1.
P01506; HCV_NS4b; 1.
P01006; HCV_NS4b; 1.
P010071; helicase_C; 1.
P000998; Viral_RdRP; 1.
                RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF----ASRQNHVSPTHY
 RPAVVPDREVLYREFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQ-
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                                                       ; Pred. No. 7.40
31; Mismatches
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NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

NON-STRUCTURAL PROTEIN NS2/EDITIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED FROM CAPSID PROTEIN C
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MATRIX PROTEIN (POTENTIAL).
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SEQUENCE FROM N.A.

Hepacivirus

NCBI_TaxID=31642;

Virus Res.

PDB; 1JXP; 14-JAN-9 MEROPS; S29.001; -. MEROPS; U39.001; -.

1A10; 25-MAR-98. 1JXP; 14-JAN-98.

InterPro; IPR001410;
InterPro; IPR002522;
InterPro; IPR002521;

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     X MEDLINE=91172826; PubMed=1848704;
X Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,
A Choo Q.-L., Richman K.H., Han J.H., Barr P.J., Weiner A.J.,
A Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,
A Bradley D. W., Kuo G., Houghton M.,
I "Genetic organization and diversity of the hepatitis C virus.",
I Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
I Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
C -!- FUNCTION. THE SMALL PROTEINS NS2B, NS2B, NS4A AND NS4B ARE.
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
C -!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (GP22) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS46 (P4); Nonstructural protein NS48 (P27); Nonstructural protein NS48 (P27); Nonstructural protein NS48 (P27); RNA-directed RNA polymerase) (EC 2.7.7.48)].
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate 1) (HCV).
Hepatitis SRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                       PIR; A39166; GNWVC3.
PDB; 1A1V; 16-FEB-99.
PDB; 1HEI; 25-NOV-98.
                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way
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NCBI_TaxID=11104;
                 MEROPS; $29.001; -. MEROPS; U39.001; -.
                                                                                                                       EMBL; M62321; AAA45676.1; -.
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE, THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN MAND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA.

PROTEIN C AND MRNA.
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Pro; IPRO02868;

Pro; IPRO02166; HCV_RdRP.

Pro; IPRO01650; Helicase C.

Pro; IPRO01650; Helicase C.

Pro; IPRO01650; Helicase C.

Pro; IPRO07095; RNA_pol_DS_PS.

Pro; IPRO07094; RNA_pol_PS_VII.

Am; PP01543; HCV_core; 1.

Am; PP01543; HCV_env; 1.

Am; PP01539; HCV_env; 1.

Am; PP01539; HCV_NS1; 1.

Pfam; PP01530; HCV_NS3; 1.

Pfam; PP01506; HCV_NS4; 1.

Pfam; PP01006; HCV_NS4; 1.

Pfam; PP01001; HCV_NS4; 1.

Pfam; PP01001; HCV_NS4; 1.

Pfam; PP01506; HCV_NS5a; 1.

Pfam; PP01506; HCV_NS5a; 1.

Pfam; PP01001; HcV_NS4; 1.

Pfam; PP01506; HCV_NS5a; 1.

Pfam; PP01506; HCV_NS5a; 1.

Pfam; PP01506; HCV_NS5a; 1.

Pfam; PP00998; Viral_RdRP; 1.

ProDom; PD186062; HCV_NS1; 1.

SMART; SM00487; DEXDC; 1.

SMART; SM00487; Coat proctein; Envertural processing services of the process of the
Query Match
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HCV_NS5a.
HCV_RdRP.
14.0%;
                                                              327197
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HCV_core.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                              ž
Score 254;
Pred. No.
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                                                                                                                                                                                      N-LINKED
                                                                                                                                                                                                                                                N-LINKED
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MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONSTRUCTURAL PROTEIN NS4A (POTENTIAL). NONSTRUCTURAL PROTEIN NS4B (POTENTIAL). RNA-DIRECTED RNA POLYMERASE (POTENTIAL)
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Matches

Similarity

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Mismatches

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78;

Gaps

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                                                                                                                                                                                                                                                                                     Kim J.L., Moryemster.....P.R.;
Murcko M.A., Lin C., Caron P.R.;
"Hepatitis C virus NS3 RNA helicase domain with a bound
"Hepatitis C virus NS3 RNA helicase domain with a bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                            -i- FUNCTION: PROTEASE NS2 IS RESPONSIBLE FOR THE
-i- FUNCTION: PROTEASE NS3 IS RESPONSIBLE FOR THE
NS3-NS4A, NS4A-NS4B, NS4B-NS5A AND NS5A-NS5B.
-i- FUNCTION: NS4A FORMS A COMPLEX WITH NS3 AND IS
                                                                                                                                                                                                                                                        Structure 6:89-100(1998)
                                                                                                                                                                                                                                                                                of unwinding.";
                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MEDLINE=98154321; PubMed=9493270; Kim J.L., Morgenstern K.A., Griffith J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97331322; PubMed=9187654;
Yao N., Hesson T., Cable M., Hong Z., Kwong A.D.,
"Structure of the hepatitis C virus RNA helicase of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic structure of the human prototype strain H of virus: comparison with American and Japanese isolates. Proc. Natl. Acad. Sci. U.S.A. 88:10292-10296(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
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01-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inchauspe G.,
       ESSENTIAL CATALYTIC precursor position,
                     FUNCTION: NSSA SEEMS TO HAVE A TRANSCRIPTIONAL ACTIVATORY ROLE. FUNCTION: NSSB IS A RNA-DEPENDENT RNA POLYMERASE THAT PLAYS AN ESSENTIAL ROLE IN THE VIRUS REPLICATION.

CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6
                                                                                                                                           ACTIVATION OF NS3.
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edee S., Lee D.H.H., Sugitani M.,
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED E SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED E LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS LIPOPROTEIN C AND MRNA. PTM: THE STRUCTURAL PROTEINS C, EI AND EZ ARE PRODUCED BY PROTEOLYTIC PROCESSING BY THE HOST SIGNAL PEPTIDASES.

SIMILARITY: THE NS2 PROTEASE BELONGS TO PEPTIDASE FAMILY U39. SIMILARITY: THE NS3 PROTEASE BELONGS TO PEPTIDASE FAMILY SESSIMILARITY: THE NS3 PROTEASE BELONGS TO PEPTIDASE FAMILY SESSIMILARITY SESSIMILARIT
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1A1V; 16-FEB-99.
1A1R; 17-JUN-98.
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); IPR002518; HCV_NS2.

); IPR004109; HCV_NS3.

); IPR00145; HCV_NS4a.

); IPR001490; HCV_NS4a.

); IPR002868; HCV_NS5a.
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IPR002522;
IPR002521;
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CHARGE RELAY SYSTEM

CHARGE RELAY SYSTEM

CHARGE RELAY SYSTEM
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NONSTRUCTURAL PROTEIN NS4B.
NONSTRUCTURAL PROTEIN NS5A.
NONSTRUCTURAL PROTEIN NS5B.
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                                                                                                                                                                                                           PROTEIN P7.
NONSTRUCTURAL PROTEIN NS2.
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RE SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RA Okamoto H., Okada S.-I., Sugiyama Y., Kurai K., Lizuka H.,

RA Okamoto H., Okada S.-I., Sugiyama Y.,

RA Machida A., Miyakawa Y., Mayumi M.;

RT "Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a human carrier comparison with reported isolates for conserved and divergent regions.";

RI "Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a human carrier comparison with reported isolates for conserved and divergent regions.";

RI J. Gen. Virol. 72:2697-2704(1991).

CC :-- FUNCTION: THE SWALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE CC HYDROPHOBIC, SUGGESTING A POSSTBLE MEMBRANE-RELATED FUNCTION.

CC :-- FUNCTION: THE SWALL PROTEINS OF FOUR PROTEIN IN the PART OF THE VIRAL RNA REPLICATION.

CC :-- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the PART OF COMPACTIVITY: N nucleoside triphosphate = N diphosphate + CC (ARA)(N).

CC :-- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + CC (ARA)(N).

CC :-- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN C AND MRNA.

CC :-- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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POLG_HCVJ6 STANDARD; PRT; 3033 AA.

AC P26660;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 41, Last annotation update)

DT 028-FEB-2003 (Rel. 41, Last annotation update)

DE Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);

Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2

DE Envelope glycoprotein F7; Nonstructural protein NS2 (P21)

DE (GP68) (GP70) (NS1); Protease NS3 (P70) (Hepacivirin)

DE (EC 3.4.22.-1); Protease/helicase NS3 (P70) (Hepacivirin)

DE (EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein

NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein

NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein

NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein

NS4B (P56) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)]
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INIT_MET 1 REMOVED FROM CAPSID PROTEIN C BY THE
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PF02907; HCV_NS;

PF01006; HCV_NS;

PF01001; HCV_NS;
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122; HCV_core.
121; HCV_core.
129; HCV_env.
13; HCV_NS1.
145; HCV_NS2.
16; HCV_NS3.
145; HCV_NS4A.
146; HCV_NS5A.
146; HCV_NS4A.
146; HCV_NS5A.
14
                                                                                                                                                                                                                                                                                                                                                                                     CAPSID PROTEIN C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).

RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
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N-LINKED
N-LINKED
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NG1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS4B (P27); Nonstructural protein NS4B (P27); Nonstructural protein NS4B (P37); Nonstructural protein NS4B (P37); Nonstructural protein NS4B (P37); Nonstructural protein NS5B (P56); Nonstructural protein NS5B (P56); Nonstructural protein NS5B (P56); SP70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate HC-JB) (HCV)
Virusas: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE rever i...

MEDLINE=92230232; PubMed=1314459;

Okamoto H., Kurai K., Okada S.-I., Yamamoto K., Lizuka H., Tanaka Fukuda S., Tsuda F., Mishiro S.;

Fukuda S., Tsuda F., Mishiro S.;

"Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis C virus genome having poor "Full-length sequence of a hepatitis" of the poor "Full-length" of t
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SEQUENCE
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Virology 188:331-341(1992)
-!- FUNCTION: THE SMALL PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.

NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the vertices polyprotein, commonly with Asp or Glu in the P6 position. Cys or Thr in P1 and Ser or Ala in P1'.

CATALYTIC ACTIVITY: N nucleoside triphosnhar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS PROTEIN A AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1619 KPTLVGPTPLLYR-----LGSVTNEVTLTHPVTKYIATCMQADLEVMTSTWVLAGGV
                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 KEKVLAFASRGN------HVSPRHYVPESEPQVVVTPDKEILYEAFDEMEE-ASKAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 KPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVESDAS---ASLPYMDETRAIAGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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3033 AA;
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                                                                                                                          BAA01761.1;
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                                                                                                                                                                                                                                    moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in wed. Usage L.
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PIR; A40250; GNWVJ8. HSSP; P27958; 1HEI.

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Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
Transmembrane; Nonstructural protein; Hydrolase; Serine protease.
Transmembrane; Nonstructural protein; Hydrolase; Serine protease.
Transmembrane; Nonstructural protein; Celi, Grom Capsid prom Capsid promesid Protein C BY THE
CELLULAR AMINOPEPTIDASE.
Transmembrane; Nonstructural PROTEIN C BY THE
CELLULAR AMINOPEPTIDASE.
Transmembrane; Nonstructural PROTEIN C BY THE
CEAIN 116 191 MATRIX PROTEIN C (POTENTIAL).
Transmembrane; Nonstructural PROTEIN NS1 (POTENTIAL).
Transmembrane; Nonstructural PROTEIN NS2 (POTENTIAL).
Transmembrane; Nonstructural PROTEIN NS4A (POTENTIAL).
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Best Local
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Pfam; PF01538; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; Viral_RdEP; 1.
ProDom; PD186062; HCV_NS1; 1.
SMART; SM00487; DEXDC; 1.
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                                                                                                                                                                                                                                               CARBOHYD
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InterPro;
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Pfam; PF01542; HCV
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; IPR000745;
; IPR001490;
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121; HCV_env.
131; HCV_NS1.
18; HCV_NS2.
19; HCV_NS3.
4CV_NS4A.
90; HCV_NS4b.
68; HCV_NS5A.
66; HCV_NS5A.
96; RNA_pol_DS_PS.
94; RNA_pol_PSvir.
V_capsid; 1
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SMART; SM00150; SFEC, J. SMART; SM00150; SFEC, J. 1.
PROSITE; PS00019; ACTININ_2; 1.
PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS50021; CH; 2.
PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00018; EF_HAND; 1.
Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Calcium-binding; Repeat; Multigene Actin-binding; Multigene Actin-binding; Multigene Actin-binding; Multigene Actin-binding; Multigene Actin-binding; Multige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF190909; AAF20064.1; -..
PIR; JC7186; JC7186.
HSSP; Q01082; 1BKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Contains 1 actin-binding domain.

-!- SIMILARITY: Contains 2 calponin-homology (CH) c

-!- SIMILARITY: Contains 2 EF-hand calcium-binding

-!- SIMILARITY: Contains 4 spectrin repeats.
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-!- FUNCTION: F-ACTIN CROSS-LIMING PROTEIN WHICH IS THOUGHT TO ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. THIS IS A BU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANC4 RAT STANDARD; PRT; 911 AA. 090X00; [16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Alpha-actinin 4 (Non-muscle alpha-actinin 4)
                                                                                                                                                                                                                                                                                            SMART; SM00033; CH; 2.
SMART; SM00054; EFh; 2.
SMART; SM00150; SPEC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00036; efhand; 2.
Pfam; PF00435; spectrin; 4.
ProDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN.
-!- SUBUNIT: HOMODIMER, ANTIPARALLEL (BY THE N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001589; Actbind actnin.
InterPro; IPR00201715; Calponin-like.
InterPro; IPR002048; EF-hand.
InterPro; IPR002017; Spectrin.
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D., Kwasnicka D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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Best Local
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090XZ0; P97394; P97395; P97396;
16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Microtubule-actin crosslinking factor 1 (Actin cross-linking family
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SEQUENCE
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REPEAT
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REPEAT
                                               Leung C.L., Sun D., Zheng M., Knowles D.R., Liem R.K.H. "Microtubule actin cross-linking factor (MACF): a hybri and dystrophin that can interact with the actin and mic cytoskeletons.";
                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 PARTIAL SEQUENCE FROM N.A. (ISOFORMS STRAIN=BALB/c; TISSUE=Brain; MEDLINE=97124842; PubMed=8954775;
                                                                                                     SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                               MACF1 OR MACF OR ACF7 OR ACLP7.
                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                   MEDLINE=20069791; PubMed=10601340;
                                                                                               STRAIN=BALB/c;
                                                                                                                        NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 79; Conserv
                                                                                                                                                                                                                                                                             TTIARTINEVENQILTRDAKGISQEQMQEFRASFNHFDKDH
                                                                                                                                                                                                                                                                                               SDASASLPYMDE---TRAIAGQFKEKVLAFASRGNHVSPRH
                                                                                                                                                                                                                                                                                                                                                        EKVQQLVPKRDHALLEEQSKQQSNEHLRRQFASQANMVGPWIQTKMEEIGRISIEMNGTL
                                                                                                                                                                                                                                                                                                                                                                                                              GNHDSPTHYVPESD-AKPAIIPDREVLYREFDEMEESQHL-----PY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                 TEKOLETIDOLHLEYAKRA-----APFNNWMESAMEDLODMFIVHTI-EEIEGLISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVLHREFDEMEEAFASRGNHVSPAHYVPESDASQAAPYIEQAQVIAHQFKEKVLAFASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHQDRVEQIAAIAQELNELDYYDSHNVNTRCQKICDQWDNLGSLTH-----SRREALEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHLPYIEQGMQLAEQFKQ-------KALAFASRQNHV-SPTHYVPESDARPAIIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I PRLERLDHLAEKFROKAS I HEAWTDGKEAMLKHRDYETATLSDIKALIRKHEAFESDLA
                                                                                                                                                                                                                                                                                                                  EDQLSHLKQYERSIVDYKPNLDLLEQQHQLIQEALIFDNKH---TNYTMEHLRVGWEQLL
                                                                                                                                                                                                                                                                                                                                     ----THYVTESDAKPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVE------
                                                                                                                                                                                                                                                                                                                                                                         --IEQ-----GMMLAEQFKQKA----LAFASRGNHVAP------
                                                                                                                                                                                                                                                                                                                                                                                             --HDQFKSTLPDADREREAIL----AIHKEAQRIAESNHIKLSGSNPYTSVTPQIINSKW
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911
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413
528
649
778
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163
177
                                                                                                                                                     (Mouse)
                                      147:1275-1286(1999).
                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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19.7%;
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SPECTRIN 1.
SPECTRIN 2.
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Pred. No. 0.9
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EF-HAND 1 (POTENTIAL)
EF-HAND 2 (POTENTIAL)
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CH 2.
POLYPHOSPHOINOSITIDE (PIP2)-BINDING
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                                                        a hybrid of dyspand microtubule
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                                                                 dystonin
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  SMART; SM00033; CH; 2.
SMART; SM00054; EFh; 2.
SMART; SM00243; GAS2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00150; SPEC; 36.
                                                                                                                                                                                                                                                                                                                         EMBL; AF150755; AAD32244.1; -.
EMBL; U67203; AAC52988.1; -.
EMBL; U67204; AAC52989.1; -.
EMBL; U67205; AAC52990.1; -.
HSSP; Q01082; 1BKR.
MGD; MGI:108559; Macf1.
        REPEAT
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                                                                                                                         PROSITE;
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PROSITE; PS00020;
PROSITE; PS50021;
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Pfam; PF00435; specti
                                                                                                                                                                                                                                                                  InterPro; IPR001589; Actbind_actnin
InterPro; IPR001715; Calponin-like.
InterPro; IPR002048; EF-hand.
InterPro; IPR003108; GAS2.
InterPro; IPR001452; SH3.
InterPro; IPR002017; Spectrin.
                                                                                                      Alternative
                                                                                                                                                                                                                                                  Pfam;
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                                                                                                                                                                                                                                                 PF00036; efhand;
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                                                                                                                                                                                                                  F00435; spectrin; 27. PD000012; EF-hand; 1
                                                                                                                       PS50002;
                                                       78
194
314
591
                                                                                                      splicing
                                                                                                                Cytoskeleton;
                                                                                                                         SH3; FAL
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ACTININ 2; FALSE_NEG
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                                                                                                                        FALSE NEG.
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                                                                         ACTIN-BINDING
CH 1.
CH 2.
SPECTRIN
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SPECTRIN
SPECTRIN
SPECTRIN
SH3.
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(BY

SIMILARITY)

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ISOId=Q9QXZO-3; Sequence=VSP_000718;
-: TISSUE SPECIFICITY: EXPRESSED MAINLY IN LUNG, E
SKELETAL AND CARDIAC MUSCLE, AND SKIN.
-: SIMILARITY: Contains 1 actin-binding domain.
-: SIMILARITY: Contains 2 calponin-homology (CH) d
-: SIMILARITY: Contains 2 EF-hand calcium-binding
-: SIMILARITY: Contains 1 SH3 domain.
-: SIMILARITY: Contains 37 spectrin repeats.
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bernier G., Mathieu M., De Repentigny Y., Vidal S.M., "Cloning and characterization of mouse ACF7, a novel dystonin subfamily of actin binding proteins."; Genomics 38:19-29(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Cytoplasmic -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: F-ACTIN-BINDING PROTEIN WHICH MAY PILINKING ACTIN TO OTHER CYTOSKELETAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9QXZ0-2; Sequence=VSP_000717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9QXZ0-1; Sequence=Displayed
                                                                         non-profit institutions as long
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                          http://www.isb-sib.
                                               Usage
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                                                                                                  SDANEQYKLISDTVGQRVDEIDAAIQRSQQYEQAADAELAWVAETKRKLMALGPIRL--E
                                                                   SDARPAIIPDREV----LHREFDEMEEAFASRGNHVSPAH----
                                     QDQTTAQLQVQKAFSIDIIRHKDSMDELFSHRGEIFSTCGEEQKAVLQEKTECLIQQYEA
                                                                                                                                                            IPQFQQ-----RQKELKKEVMEHRLVL----DTVNEVSHVLLELVPWRAREGLDKRV
        ----SQAAPYIEQAQVIAHQFKEKVLAFASRGNHDSPTHYVPESDAKPAIIP----DRE
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1882
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7 AA; 607972
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                                                                                                                                                                                                                                      6.6%;
                                                                                                                                                                                                                           76;
                                                                                                                             --IEQGMQLAEQFKQKA---LAFASRQNH----VSPTHYVPE
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SPECTRIN 10.
SPECTRIN 11.
SPECTRIN 11.
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SPECTRIN 37.
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Q -> H (IN REF. 2).
MW; 5DE4FF5A6514BFFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           TLPWNLPLHEOKKRKSODSVLDPAERAVVRVADERDRVOKK
TFTKWYNKLLMKVRKH INDLYEDLRDCHKLVIS ILEVLSGIK
LPREKGRMFHELQNVOJALDFKJROVKLVISIRNDDITDG
LPREKGRMFHELQNVOJALDFKJROVKLVISIRNDDITDG
MPKLTLGLIWTI ILHFO - MGNSLGCVKEPKES IAVPEK
APIS PKKRVRF FKRKWRGKKILTPEASHREEALEGTGV LEET
ETLTKLTARLLEKEPGVGGAEHPPSDIF LPGGSAPNSGVGDO
GMIVOVKESFOAEI OTAHLLLENESSVVGGAMDSLEEGMTV
                                                                                                                                                                                                                                        Score 120.5; I
Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 X 4 AA TANDEM REPEATS OF [GS]-S-R-[AR].
MSSSDEETLSERSCRSERSCRSERSYRSERSGSLSPCPPGD
TLPWNLPLHEQKKRKSQDSVLDPAERAVVRVA -> EKEFV
QAYEDVLERYK (in isoform 1).
/FTId=VSP_000717.
MSSSDEETLSERSCRSERSCRSERSYRSERSGSLSPCPPGD
                                                                                                                                                                                                                                                                                                                               LVSCKGPIMPASQSDLSVSGITVSILPSSSGYGSDGLRLHG
IRPEDTEPEKTSTPFSEEDGTLSLE (in isoform 3).
/FTId=VSP_000718.
                                                                                                                                                                                                                                                                                                                                                                               IAHLLDNPAERNCEKSVSQLVEFPRTASCSSRAVLLPLQGE
TAVEQGGTLLRHRHRSSTLPRTDYPSETVDQDQPSEGWSVG
GRTKSVPSAPPTGSWIAKCSVASSIPKQSGDPIHTEPTHVG
                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                        124;
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P57780;
16-OCT-2001
Pfam; PF00435; spectrin; 4.
ProDom; PD00012; EF-hand; 1.
SMART; SM00033; CT; 2.
SMART; SM00054; EFh; 2.
SMART; SM00150; SPEC; 3.
                                                              Pfam; PF00036;
Pfam; PF00435;
                                                                                                                                                                                         EMBL; AJ289242; CAC10069.1; HSSP; Q01082; 1BKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                               efhand; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMODIMER, ANTIPARALLEL (BY SIMILARITY).
-!- SIMILARITY: Contains 1 actin-binding domain.
-!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains
MGD; MGI:1890773; Actn4.
InterPro; IPR001589; Actbind actnin
InterPro; IPR001715; Calponin-like.
InterPro; IPR002048; EF-hand.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomics 68:152-160(2000).
-!- FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH IS THOUGHT TO ANCHOR ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. THIS IS A BUNDLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dear T.N., Meier N.T., Hunn M., Boehm T.; "Gene structure, chromosomal localization and expression pattern Capn12, a new member of the calpain large subunit gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-actinin 4 (Non-muscle alpha-actinin 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20422668; PubMed=10964513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPMLETLENLSSRLRMP---PLIPAEVDK--IRECISDNKSAT--VELEKLQPSFEALKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                       actnin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                             EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
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RESULT 12
PLE1_CRIGR
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CA_BIND
CA_BIND
SEQUENCE
                                                                                                                                                                                                                                        PLE1 CRIGR STANDARD; PRT; 4473 AA. 09J155; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 19-OCT-2001 (Rel. 40, Created) 19-OCT-2001 (Rel. 40, Last sequence update) 19-OCT-2001 (Rel. 40, Last annotation update) 19-OCT-2001 (Rel. 40, Las
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REPEAT
REPEAT
                                     Clubb B.H., Cl
Goldman R.D.;
                                                        SEQUENCE FROM N.A.
MEDLINE=20334248; PubMed=10873583;
Clubb B.H., Chou Y.-H., Herrmann H.,
                                                                                                                                                                            Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Veri
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                             Cricetulus.
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Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00019; ACTININ 1;
PROSITE; PS00020; ACTININ 2;
PROSITE; PS50021; CH; 2.
                  "The 300-kDa intermediate filament-associated protein (IFAP300) is
                                                                                                                                      NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQ-----GMMLAEQFKQKA-----LAFASRGNHVAP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSPTHYVPESD-AKPAIIPDREVLYREFDEMEESQHL-----PY------I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLETIDQLHLEYAKRA-----APFNNWMESAMEDLQDMFIVHTI-EEIEGLISA--H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRVEQIAAIAQELNELDYYDSHNVNTRCQKICDQWDNLGSLTH-----SRREALEKTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYIEQGMQLAEQFKQ------KALAFASRQNHV-SPTHYVPESDARPAIIPDREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LERLDHLAEKFROKASIHEAWTDGKEAMLKORDYETATLSDIKALIRKHEAFESDLAAHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SDASASLPYMDE---TRAIAGQFKEKVLAFASRGNHVSPRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -THYVTES----DAKPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQLVPKRDHALLEEQSKQQSNEHLRRQFASQANMVGPWIQTKMEEIGRISIEMNGTLEDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DQFKSTLPDADREREAIL----AIHKEAQRIAESNHIKLSGSNPYTTVTPQIINSKWEKV
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912
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414
529
650
779
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164
178
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267 ACT
155 CH
267 CH
193 POL
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519
640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 114.5;
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF-HAND 1 (POTENTIAL)
EF-HAND 2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ig; Repeat; Multigene family.
ACTIN-BINDING (BY SIMILARITY).
CH 1.
CH 2.
CH 2.
POLYPHOSPHOINOSITIDE (PIP2)-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07AA9C92AC228B5A CRC64;
                                                          Svitkina T.M.,
                                                                                                                                                                              Vertebrata; I
thi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                             filament-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                            Euteleostomi;
; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
                                                            Borisy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912;
                                                            G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46
    STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT
C ALSO IN THE REGULATION OF THEIR DYNAMICS.
C -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
C -!- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH
C AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
C AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
C -!- PTM: PHOSPHORYLATED BY CDC2, REGULATES DISSOCIATION FROM
INTERMEDIATE FILAMENTS DURING MITOSIS.
C -!- SIMILARITY: Contains 1 actin-binding domain.
C -!- SIMILARITY: Contains 2 plectin repeats.
C -!- SIMILARITY: Contains 4 spectrin repeats.
C -!- SIMILARITY: Belongs to the plakin or cytolinker family.
C -!- SIMILARITY: Belongs to the plakin or cytolinker family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00307; CH; 2.
Pfam; PF00681; Plectin; 20.
SMART; SM00033; CH; 2.
SMART; SM00250; PLEC; 34.
PROSITE; PS00019; ACTININ 1; P.
PROSITE; PS00020; ACTININ-2; F.
PROSITE; PS50021; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation.
NON TER 1
DOMAIN 1
DOMAIN 1260
DOMAIN 2545
DOMAIN 41
DOMAIN 41
                    REPEAT
REPEAT
REPEAT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed to the Entropean Bioinformatics Institutions as long as its content use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR0011101; Plectin_repeat.
InterPro; IPR002017; Spectrin.
Pfam; PF00307; CH; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF260753; AAF70372.1; -. HSSP; Q01082; 1BKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping of a single phosphorylation site.";
J. Biol. Chem. 271:8203-8208(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malecz N., Foisner R., Stadler C., Wiche G.; "Identification of plectin as a substrate of
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96215219; PubMed=8626512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. Biophys. Res. Commun. 273:183-187(2000)
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FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES ANI MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES (HEMIDESMOSOMES, MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND
                                                                                                                                                                                                                                                                             1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Structural protein; Cytoskeleton; Actin-binding;
189
508
613
719
719
1244
2548
22652
2652
2708
27728
27942
2980
27942
33054
33054
3349
                                                                                                                                                                                                                                                                                                                                                                                 1259
2544
4473
192
74
                PLECTIN 1.
PLECTIN 2.
PLECTIN 3.
PLECTIN 4.
PLECTIN 5.
PLECTIN 6.
PLECTIN 7.
PLECTIN 8.
PLECTIN 10.
PLECTIN 10.
PLECTIN 11.
PLECTIN 11.
                                                                                                                                                                                                                                                                                                                                                          ACTIN-BINDING.
CH 1.
CH 2.
                                                                                                                                                                                                                                                                                                  SPECTRIN
SPECTRIN
SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL
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COILED COIL
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                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           ROD DOMAIN
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a collaboration -MBL outstation outstation

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AAC4 HUMAN STANDAN,
O43707; O76048;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Allsschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Allsschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Allsschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Allsschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Wallan N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Hala S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Willalon D.K., Maru A., Young A.C., Shevchenko Y., Bouffard G.G., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Pyroc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                           "Mutations in ACTN4, encoding alpha-actinin-4, cause segmental glomerulosclerosis";
Nat. Genet. 24:251-256(2000).
-i- FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH IS ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. T
                                                                                                                                                                                                                                                                                                                                    MEDLINE=20164321; PubMed=10700177;
Kaplan J.M., Kim S.H., North K.N., Rennke H., Correia
Tong H.-Q., Mathis B.J., Rodriguez-Perez J.-C., Allen
Beggs A.H., Pollak M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-218 FROM N.A.
Isogai T., Otsuki T., Sugiyama T.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ
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Chiba H.,
J. Cell Bi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-170
Ottenwaelder B., C
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suppresses tumorigenicity of human neuroblastoma
Oncogene 19:380-386(2000).
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MEDLINE=98177166; PubMed=9508771;
Vamada T., Endo R., Ino
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Nikolopoulos S.N., Spengler B.A., Kisselbach
Biedler J.L., Ross R.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS FSGS1 GLU-255; ILE-259 AND
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PROTEIN.
SUBUNIT: HOMODIMER, ANTIPARALLEL (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. COLOCALIZES WITH
ACTIN STRESS FIBERS. NUCLEAR TRANSLOCATION CAN BE INDUCED BY THE
P13 KINASE INHIBITOR WORTMANNIN OR BY CYTOCHALASIN D. EXCLUSIVELY
LOCALIZED IN THE NUCLEUS IN A LIMITED NUMBER OF CELL LINES (BREAT)
CANCER CELL LINE MCF7, ORAL FLOOR CANCER IMC2, AND BLADDER CANCER
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Hirohashi :
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(BREAST CANCER

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Pfam; PF00435; spectrin; 4.
ProDom; PD000012; EF-hand; 1.
SMART; SM00033; CH; 2.
SMART; SM00034; EFh; 2.
SMART; SM00150; SPEC; 3.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00019; ACTININ 1; 1.
PROSITE; PS00021; CH; 2.
PROSITE; PS00021; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 604638; -.
MIM; 603278; -
GO; GO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- DISEASE: Cycoplasmic localization of ACTN4 may be associated with cancer metastases due to enhanced cell motility.
-!- DISEASE: Defects in ACTN4 are the cause of focal segmental glomerulosclerosis 1 (FSGS1) [MIM:603278], a common renal lesion characterized by increased urinary protein excretion and decreasing kidney function. Renal insufficiency often progresses to end-stage renal failure, a highly morbid state requiring either dialysis therapy or kidney transplantation. FSGS is defined by the presence of segmental sclerosis in glomeruli, and is seen in all ethnic groups, although it is particularly common in individuals of african descent. FSGS occurs as an isolated primary condition or secondary to disorders as HIV infection, obesity, hypertension and diabetes. FSGS may also be inherited as a mendelian trait.
-!- SIMILARITY: Contains 1 actin-binding domain.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
-!- SIMILARITY: Contains 4 spectrin repeats.
-!- CAUTION: REF: 3 SEQUENCE DIFFERS FROM THAVE CORRECTED. THE REMAINING SEQUENCE CONFLICTS INCLUDE BOTH SMALL FRAMESHIFTS AS WELL AS POINT THE CHAPPE MAMALIAN SEQUENCEING ERRORS WHEN COMPARED WITH THE OTHER MAMALIAN SEQUENCEING ERRORS WHEN COMPARED WITH
    REPEAT
REPEAT
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DOMAIN
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Pfam; PF00036; efhand; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                      ତ୍ର ତ
                                                                                                                                                                                                                                                                                                                                       GO; GO:0007125; P:invasive growth; InterPro; IPR001589; Actbind actnin InterPro; IPR001715; Galponin-like. InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D89980; BAA24447.1; ALT INIT.
EMBL; U48734; AAC17470.1; ALT FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:166; ACTN4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; Q01082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                           Actin-binding;
                                                                                                                                                                                                                                                                                                                          interPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                            GO:0015629; C:actin cytoskeleton; TAS. GO:0005737; C:cytoplasm; TAS. GO:0005634; C:nucleus; TAS. GO:0005200; F:structural constituent of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KU7).
TISSUE SPECIFICITY: Widely expressed DISEASE: Cytoplasmic localization of
                                                                                                                                                                                                                                                                                                                                                                                                 GO:0006928; P:cell motility; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE OTHER MAMMALIAN SEQUENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC005033; AAH05033.1; -
AL047603; -; NOT_ANNOTATED_CDS
AU118403; -; NOT_ANNOTATED_CDS
                                                                                                                      mutation; Nuclear protein
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528
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                                                                                                                                    Calcium-binding; Repeat; Multigene family;
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                                                                           ACTIN-BINDING CH 1.
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POLYPHOSPHOINOSITIDE (PIP2)-BINDING SPECTRIN 1. SPECTRIN 2. SPECTRIN 3.
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PLE1_HUMAN
   ROCCOS COTTO
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DLE1_HUMAN STANDARD; PRT; 4684 AA Q15149; Q15148; Q1640; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)

4684 AA

272

690

158 525 86

(PCN) (Hemidesmosomal

protein

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;

Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostomi;

Homo sapiens (Human) Plectin 1 (PLTN)

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Matches 79
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NEVENQILTRDAKGISQEQMQEFRASFNHFDKDH
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                                                                                 KQYERSIVDYKPNLDLLEQQHQLIQEALIFDNKH----TNYTMEHIRVGWEQLLTTIARTI
                                                                                                                            VTESDAKPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVE--
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S-> P (in FSGS1).
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C-> S (IN REF. 3).
V-> I (IN REF. 3).
S-> L (IN REF. 4).
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I -> SV (IN REF. 3).
I -> I (IN REF. 3).
I -> II (IN REF. 3).
O -> QO (IN REF. 3).
GR -> A (IN REF. 3).
A -> T (IN REF. 3).
MISSING (IN REF. 3).
AVP -> GVR (IN REF. 3).
AVP -> GVR (IN REF. 3).
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Pred. No. 3.3;
66; Mismatches
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EF-HAND 2 (POTENTIAL).
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(in FSGS1).
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CRC64;
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Uitto J

VARIANT

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21090821; PubMed=11159198; Bauer J.W., Rouan F., Kofler B., Rezniczek G.A., Kornacker I., Muss W., Hametner R., Klausegger A., Huber A., Pohla-Gubo G., Wiche G., Uitto J., Hintner H.; Wiche G., Uitto J., Hintner H.; "A compound heterozygous one amino-acid insertion/nonsense mutation the plectin gene causes epidermolysis bullosa simplex with plectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97049959; PubMed=8894687; Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Hachisuka H., Nishikawa T., McLean W.H.I., Uitto J. Hachisuka H., Nishikawa T., McLean W.H.I., Uitto J. "Homozygous deletion mutations in the plectin gene with epidermolysis bullosa simplex associated with muscular dystrophy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deficiency."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McLean W.H.I., Pulkkinen L., Smith F.J.D., Rugg E.L., Bullrich F., Burgeson R.E., Amano S., Hudson D.L., OwanGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96312447; PubMed=8698233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome localization (8q24)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96210632; PubMed=8633055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Pathol. 158:617-625(2001).

J. Pathol. 158:617-625(2001).

J. Pathol. 158:617-625(2001).

J. Pathol. 158:617-625(2001).

FILAMENTS WITH MICROTUBULES AND FILAMENTS TO DESMOSOMES ON MICROFILAMENTS AND ANCHORS LINTERMEDIATE FILAMENTS TO DESMOSOMES OR HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO MEMBRANE COMPLEXES IN MUSCLE. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS. SUBUNIT: HOMODIMER OR HOMOTETRAMER.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q15149-2; Sequence=VSP_005030;
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                                                                                                                                                                                                                                                                                                                                                                           Sequence=VSP_005030, VSP_005031; Y: WIDELY EXPRESSED WITH HIGHEST LEVELS
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Owaribe K.,
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ProDom; PD006662; S10_plectin_N; 1.
SMART; SM00033; CH; 2.
SMART; SM00250; PLEC; 34.
SMO0251TE; PS000019; ACTININ_1; FALSE_NI
PROSITE; PS00002; ACTININ_2; FALSE_NI
PROSITE; PS00021; CH; 2.
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EMBL; U53204; AAB05427.1; -.
EMBL; U63610; AAB05428.1; -.
EMBL; U63609; AAB05428.1; JOINED.
EMBL; X97053; CAA65765.1; -.
EMBL; X97053; CAA65765.1; -.
FIR; C59404; A59404.
HSSP; Q01082; 1BKR.
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Pfam; PF00681; Plectin; 19.
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Genew; HGNC:9069; PLEC1.
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to license@isb-sib.ch).
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56 AEQFKQKALAFASRQNHVSPTHYVPESDARPAIIPDREVLHREFDEMEEAFASRGNHVSP 115
                                                                                                                                                                                                                                                                                                                                                                 71;
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                                         RDKDNTORFLQEEAEKMKOVAEEAARLSVAAQEAARLRQLAEEDLAQORALAEKMLKEKM 2453
                                                                    RGNHVSPRHYVPESEPQVVVTPDKEILYEAFDE---MEEASKAALIEEGQRMAEMLKSKI
                                                                                                                       DKEVLYQQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQFKEKVLAFAS
                                                                                                                                                   ALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTTLRLQ
                                                                                                                                                                           EVLYREFDEMEESOHLPYIEOGMMLAEOFKOKALAFASRGNHVAPTHYVTESDAKPALVP
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Pred. No. 24;
63; Mismatches
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4 X 4 AA TANDEM I
PHOSPHORYLATION
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GVTNLQVMRAMASLRARGLVRETFAWCHFFWYLTNEGIAHL
RQYLHLPPEIVAASLQRVRRPVAMVMPARRTPHVQAVQGPL
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RPGPEPAPAT -> MSGEDAEVRAVSEDVSNGSSGSPSPGD
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ISOIGEP30427-4; Sequence=VSP_005052;

ITISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN SKELETAL MUSCLE AND LOWEST IN THYMUS.

IDOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH VINENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-AND THE C-TERMINUS CAD BIND INTERAIN BETA-4.

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).

SIMILARITY: Contains 1 actin-binding domain.

SIMILARITY: Contains 2 calponin-homology (CH) domains.

SIMILARITY: Contains 3 plectin repeats.

SIMILARITY: Contains 4 spectrin repeats.

SIMILARITY: Contains 4 spectrin repeats.

SIMILARITY: Contains 4 spectrin repeats.
    Of variants with distinct first coding exons and rodless isoforms.";
Genomics 42:115-125(1997).

-I. FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTUBULES AND MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSOMES OR HEMIDESMOSOMES. MAY BE INVOLVED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE REGULATION OF THEIR DYNAMICS.

-I. SUBUNIT: HOMODIMER OR HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Glial tumor;
MEDLINE=97321050; PubMed=9177781;
Elliott C.E., Becker B., Oehler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLE1_RAT STANDARD; PRT; 4687 AA P30427; 0088879; 008880; 008880; 01-APR-1993 (Rel. 25, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                     <del>:</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A. (ISOFORMS SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96210632; PubMed=8633055;
Liu C.-G., Maercker C., Castanon M.J., Hav
"Human plectin: organization of the gene,
chromosome localization (8q24).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coiled coil
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Hauptmann R., Stratowa C., Stewart M.,
"Cloning and sequencing of rat plectin indicates a 466-kD polypeptide
chain with a three-domain structure based on a central alpha-helical
                                                                                                                                                                                                                                                                                                                                                                                                                                    Wiche G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Glial tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91268156; Pul
Wiche G., Becker B.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                         "Plectin transcript diversity: identification and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Biol. 114:83-99(1991).
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                                                                                                                                                                                          Name=4;
                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                       IsoId=P30427-3;
                                                                                                                                                                                                                                IsoId=P30427-2;
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                                                                                                                                                                                                     Sequence=VSP_005051;
                                                                                                                                                                                                                              Sequence=VSP_005050,
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InterPro; IPR005326; S10 plectin.
InterPro; IPR0052017; Spectrin.
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Pfam; PF00681; Plectin; 21.
Pfam; PF00681; Plectin; 1.
ProDom; PD006662; S10 plectin; 1.
ProDom; PD006662; S10 plectin; 1.
ProDom; PM006662; S10 plectin; 1.
SMART; SM00013; CH; 2.
SMART; SM000150; SPEC; 33.
SMART; SM000150; SPEC; 6.
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Search completed: July 25, 2003, 13:10:14
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ALIGNMENTS

A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 73 as Pro, and TTC for residue 77 as Ser

A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; s
F;16-191/product: empelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein N #status predicted <NS1>
F;300-729/Product: nonstructural protein NS1 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS1 #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1312-1317/Region: nucleotide-binding motif A (P-loop)
F;312-1317/Region: nucleotide-binding motif A (P-loop)
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;163-2013/Product: nonstructural protein NS4a #status predicted <N4A>
F;163-2013/Product: nonstructural protein NS5 #status predicted <NS5>
F;1014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate genome polyprotein - hepatitis C virus (isolate JK1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstr
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
A;Variety: isolate JK1
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001
C;Accession: S18030; S33570; A48332; S18029
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: A whole genome of hepatitis C virus cDNA was isolated from a single paragraph of the submer: S18028 A;Molecule type: genomic RNA
A;Residues: 1-3010 <HON>
A;Residues: 1-3010 <HON>
A;Cross-references: EMBL:X61596; NID:g59478; PIDN:CAA43793.1; PID:g59479
A;Experimental source: isolate JK1 from an individual
A;Experimental source: isolate JK1 from an individual
R;Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
Arch. Virol. 128, 163-169, 1993
A;Title: Sequence analysis of putative structural regions of hepatitis C virus isola
A;Reference number: A48332; MUID:93119270; PMID:8380322
A;Accession: S33570 S A;Molecule type: genomic RNA
A;Residues: 1-547,'T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOW>
A;Residues: 1-547,'T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOW>
A;Cross-references: EMBL;X61591
A;Note: this sequence is inconsistent with the nucleotide translation A; Accession: S18030 S18030 Matches Query Match Best Local 23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF----ASRQNHVSPTHY 87; Similarity Conservative 14.5%; 27; Score 263; DB 1; Pred. No. 3.1e-09; ?7; Mismatches 74 74; Length 3010; Indels 80; Gaps carbohydrate 78

11;

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R;Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S
Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A;Title: Molecular cloning of the human hepatitis C virus genome
A;Reference number: A39253; MUID:91088550; PMID:2175903
A;Accession: A39253
                                                                                                                                                                                                                                     F:1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>F;196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,
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A; Residues: 2650-2707 < KA2>
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A; Accession: PS0086
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N;Contains: capsid protein C; envelope protein M; major envelope
protein NS4a; nonstructural protein NS4b; nonstructural protein
C;Species: hepatitis C virus
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;Kato, N.; Ohkoshi, S.; Shimotohno, K.
;Kato, Upn. Acad. 65B, 219-223, 1989
;Title: Japanese isolates of the non-A, non
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 19-Jan-2001;Accession: A39253; PS0086
                                                                                                                                                                                        Local Similarity
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                                                                  VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                    RPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                                                                                                    RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
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                                                                                                                                                                          Conservative
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                                  VVESKWRALEVFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                                                                                                                                        28;
                                                                                                                                                                                      Score 260; DB 1;
Pred. No. 4.9e-09;
                                                                                                                                                                        Mismatches
   -ASRGNHDSPTHYVPESDAKPAI
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N;Contains: capsid protein C;
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A; Residues: 1-513 < OK2>
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F;192-389/Product: major envelope protein E #status predicted < F;390-729/Product: nonstructural protein NS1 #status predicted F;730-1006/Product: nonstructural protein NS2 #status predicted F;730-105/Product: hepacivirin #status predicted <NS3> F;1007-1615/Product: hepacivirin #status predicted <NS3> F;1230-1237/Region: nucleotide-binding motif A (P-loop) F;1312-1317/Region: nucleotide-binding motif B
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C,Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolase; nucleotide binding;
C;Z-115/Product: capsid protein C #status predicted <CPC>
F;2-115/Product: envelope protein M #status predicted <EPM>
F;116-191/Product: envelope protein M #status predicted <EPM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: genomic RNA
A;Residues: 1-3011 <OKA>
A;Residues: 1-3011 <OKA>
A;Coss-references: EMBL:D10749; NID:g221586; PIDN:BAA01582.1; PID:g221587
A;Ckamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, Jpn. J. Exp. Med. 60, 167-177, 1990
A;Title: The 5'-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712
A;Accession: PC1285
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submitted to the EMBL Data Library,
A;Reference number: S40770
A;Accession: S40770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:D00831; NID:g221511; PIDN:BAA00705.1;
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protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHV-SPTH
AGYGAGVAGALVAFKIMSGELPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA
                                                                                                                                                                                                                                                                                                                               YVPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ---
                                                                                                                                 FTAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGSGLAGAAVGSVGLGRVLVDIL
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                                                               IPDREVLYREFDEMEESQHL--PYIEQGMML-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 259; DB 1;
Pred. No. 5.7e-09;
8; Mismatches 75
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Gene 105, 167-172, 1991
A;Title: Two French genotypes of hepatitis C virus: homology A;Reference number: PS0326; MUID:92039028; PMID:1718820
A;Accession: PS0326
                                                                                                          polyprotein - hepatitis C virus (isolate Fla) (fragments) C;Species: hepatitis C virus C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_C;Accession: PS0326 R;Li, J.S.; Tong, S.P.; Vitvitski, L.; Lepot, D.; Trepo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA
A; Residues: 1-3010 < CHE>
7ross-references: GB: M84754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 188, 102-113, 1992
A;Title: The Talwanese hepatitis C virus genome: sequence determination A;Reference number: A400244; MUID:92230206; PMID:1314449
A;Accession: A40244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome polyprotein - N; Contains: capsid pr
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1616-1862/Product: nonstructural protein NS4b #status predicted <N4A>
;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
;196,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;1863-2013/Product: nonstructural;2014-3010/Product: nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;192-389/Product: major envelope protein E #status predicted <MEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Accession: A40244
;Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: hepatitis C virus
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116-191/Product: envelope protein M #status predicted <EPM>
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                                                                                         J.S.; Tong, S.P.; Vitvitski, L.; Lepot, D.; Trepo,
LO5, 167-172, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                     LVDMVAGYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVD 1907
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Pred. No. 6.6e-09;
9; Mismatches 69; Indels 9
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protein M; hepacivirin (EC 3.4.21.98)
                                                                                                                                                         30-Jun-1992 #text_change
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A;Note: this sequence corresponds to nonstructural protein NS3 A;Note: translation of the nucleotide sequence is not complete C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: polyprotein
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                 F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MED>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;300-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
                                                                                                                                                                                                             F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>F;1663-2013/Product: nonstructural protein NS4a #status predicted <N4B>F;2604-3010/Product: nonstructural protein NS5 #status predicted <NS5>F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Structure and organization of the hepatitis C virus A;Reference number: A38465; MUID:91140698; PMID:1847440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Takamizawa, A.; Mori, C.; Fuke, I.;
J. Virol. 65, 1105-1113, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: A38465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; 2-115/Product: capsid protein C #status predicted <CPC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: hepatitis C virus genome polyprotein
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Best Local
                                                                                                          Matches
                                                                                                                                                     Query Match
1691 RPAIVPDRELLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
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                                               RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGRVGLGKVLVDILA 404
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Pred. No. 8.6e-10
                                                                                                                                 Score 256; DB 1
Pred. No. 9e-09;
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                                                                                                                                                       Length 3010;
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VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ---

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C;Date: 19-May-2000 t
C;Date: 19-May-2000 t
C;Accession: A45573
R;Tanaka, T.; Kato, N
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; glycoprotein; hydrolass; nucleotide binding; P-loop; poly;
E;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MED>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS1>
F;730-106/Product: hepacivirin #status predicted <NS2>
F;1007-1615/Product: hepacivirin #status predicted <NS2>
F;1030-1237/Region: nucleotide-binding motif A (P-loop)
F;1316-1319/Region: DEXH motif
F;1316-1319/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-3010 <TAN>
A;Cross-references: GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1; PID:g221613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
A45573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: A;Reference number: A45573; MUID:92295714; PMID:1318627
A;Accession: A45573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome polyprotein - hepatitis C virus (strain JT)

N ntains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)

ein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C. ecies: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: HCV-JT
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1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
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Best Local
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                                                                                                                                                                                                                                              1794
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                                                                                                                                                                                                                                                                                                                                                                                                                 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
QWMNRLIAFASRGNHVSPTHYVPESDA 1940
                                                                                                                                                                                                                                                                                                                                                        ---AEAAAPVVESR-----WRALEAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                     QFKQKALAFASRGNHVAPTHYVTESDA
                                                                                                                                                                                                                                    TASITSPLTTONTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAIGSIGLGKVLVDILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPAVVPDREVLYREFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQ-----
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                                                                                                                   GYGAGVAGALVAFKVMSGEAPSAEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV
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                                                                                                                                                                         QWMNRLIAFASRGNHVSPTHYVPESDA 1940
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                                                                                                                                                                                                                                                                                                -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------
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39-53, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IPDREVLYREFDEMEESQHL--PYIEQGMML-----
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31.5%;
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Pred. No. 9e-09;
*** marches 74;
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A;Residues: 1577-1633 <CH2>
A;Residues: 1577-1633 <CH2>
A;Residues: 1577-1633 <CH2>
A;Experimental source: isolates E-bl7
C;Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstru
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstru
F;1-115/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MEE>
F;390-729/Product: nonstructural protein NS1 #status predicted <NS1>
F;1007-1615/Product: honstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: honstructural protein NS2 #status predicted <NS3>
F;103-105/Product: honstructural protein NS2 #status predicted <NS3>
F;103-1237/Region: nucleotide-binding motif A (P-loop)
F;312-317/Region: DEXH motif
F;3136-3139/Region: DEXH motif
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
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A;Residues: 1-3011 <CHO>
A;Residues: 1-3011 <CHO>
A;Residues: 1-3011 <CHO>
A;Cross-references: GB:M62321; NID:g329873; PIDN:AAA45676.1; PID:g329874
A;Cross-references: GB:M62321; NID:g329873; PIDN:AAA45676.1; PID:g329874
A;Chan, S.W.; McComish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap
J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship
A;Reference number: PQ0393; MUID:92288871; PMID:1318939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome polyprotein - hepatitis C virus (strain HCV-1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonst
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 19-Jan-2001
C;Accession: A39166; P00403; P004040
R;Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A;Title: Genetic organization and diversity of the hepatitis C virus.
A;Reference number: A39166; MUID:91172826; PMID:1848704
A;Accession: A39166
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A; Residues: 1577-1633 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: DDBJ:D10128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PQ0403
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                                                                                                                                                                                                                                                                                                                                                                                                                 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1691 KPAIIPDREVLYREFDEMEECSOHLPYIEQGMMLAEQFKQKALGLLQTASRQAEV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                     QWMNRLIAFASRGNHVSPTHYVPESDA 1940
                                                                                                    QFKQKALAFASRGNHVAPTHYVTESDA
                                                                                                                                                                   GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                                                                                                                                                                                       TAAVTSPLTTSOTLLENILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLIDILA
                                                                                                                                                                                                                                                                                                                                                  -AQVIAHQFKEKVLAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                                                                                                                                                                                                                                                                                                       ---IAPAV------QTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                              -IPDREVLYREFDEMEESQHL--PYIEQGMML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                               -ASRGNHDSPTHYVPESDAKPAI
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78;

Gaps

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201 1853 170 1793

133

1745

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A;Note: neither amino acid nor nucleotide sequence is given
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructu:
F;1-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <AMES>
F;190-389/Product: major envelope protein NS1 #status predicted <AMES>
F;390-729/Product: nonstructural protein NS1 #status predicted <AMS2>
F;300-1006/Product: nonstructural protein NS2 #status predicted <AMS2>
F;1007-1615/Product: hepacivirin #status predicted <AMS3>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;3312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <AMA>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <AMA>
F;1863-2013/Product: nonstructural protein NS5 #status predicted <AMB>
F;1916,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,:
RESULT 10
JO1366
polyprotein - hepatitis C virus (French isolate)
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-199
C;Accession: JQ1366
R;Kremsdorf, D:, Porchon, C.; Kim, J.P.; Reyes, C
J. Gen. Virol. 72, 2557-2561, 1991
A;Title: Partial nucleotide sequence analysis of
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A;Cross-references: GB.M67463; NID:g329737; PIDN:AAA45534.1; PID:g329738
R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince
Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991
Title: Genomic structure of the human prototype strain H of hepatitis C
aference number: A41546; MUID:92052256; PMID:1658800
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A;Accession: A36814
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
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Matches 86
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                            Porchon, C.; Kim, J.P.; Reyes, G.R.; 2, 2557-2561, 1991
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Pred. No. 3.6e-08;
Pred. No. 77;
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                                                                                                                                                                  (fragments)
  French hepatitis
                                                                                                         #text_change 17-Nov-2000
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genome polyprotein
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F;1011-1619/Product: nepacryrry mounts.
F;1316-1321/Region: nucleotide-binding motif B
F;1310-1323/Region: DEXH motif
F;1320-1323/Region: DEXH motif
F;1620-1866/Product: nonstructural protein NS4a #status predicted <N4B>
F;1620-1866/Product: nonstructural protein NS4b #status predicted <N4B>
F;1867-2017/Product: nonstructural protein NS5 #status predicted <N05>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <N05>
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A;Accession: JQ1303
A;Molecule type: genomic RNA
A;Residues: 1-3033 <OKA>
A;Residues: 1-3033 <OKA>
A;Residues: 1-3033 <OKA>
A;Residues: 1-3033 <OKA>
A;Experimental source: isolate HC-J6 from a Japanese individual
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; serine pr
C;Keywords: ATP; glycoprotein; hydrolase; P-loop; polyprotein; serine pr
F;2-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <EPM>
F;192-389/Product: major envelope protein E #status predicted <MEE>
F;192-389/Product: major envelope protein E #status predicted <MEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;390-733/Product: nonstructural protein NS1 #status predicted < F;734-1010/Product: nonstructural protein NS2 #status predicted F;1011-1619/Product: hepacivirin #status predicted <NS3>
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A;Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated A;Reference number: JQ1303; MUID:92044440; PMID:1658196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision
C;Accession: JQ1303
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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A;Accession: JQ1366
A;Molecule type: genomic RNA
A;Residues; 1-716 <KRE>
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; polyprotein
C;Reywords: glycoprotein; polyprotein
C;Reywords: glycoprotein; polyprotein
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IEEGORMAEMLKSKIO 352
                                                              LAAVAAYCLATGCVCIIGRLHVNQR-
                                                                                                                                                                                        KPTLVGPTPLLYR-----LGSVTNEVTLTHPVTKYIATCMQADLEVMTSTWVLAGGV
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44.1%; Pred. No. 2.9e-05;
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No. 2.6e-06;
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C virus

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genome polyprotein - hepatitis C virus (isolate EUH1480) N;Contains: capsid protein C; envelope protein M; hepacivirin protein NS4a; nonstructural protein NS4b; nonstructural prote C;Species: hepatitis C virus C;Jate: 19-May-2000 #sequence_revision 19-May-2000 #text_chang.C;Accession: JC5620
        R;Chamberlain, R.W.; Adams, N.J.;
B.ochem. Biophys. Res. Commun. 23
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F;192-199/Product: major envelope protein E #status predicted <MEE>
F;390-733/Product: nonstructural protein NS1 #status predicted <NS1>
F;394-1010/Product: nonstructural protein NS2 #status predicted <NS1>
F;1011-1619/Product: hepacivirin #status predicted <NS2>
F;1024-1241/Region: nucleotide-binding motif A (P-loop)
F;1336-1321/Region: DEXH motif
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R;Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohnd Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A;Title: Distribution of plural HCV types in Japan.
A;Reference number: PQ0554; MUID:92068204; PMID:1720309
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R;Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamo Virology 188, 331-341, 1992
A;Title: Full-length sequence of a hepatitis A;Reference number: A40250; MUID:92230232; PAA;Accession: A40250
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A;Molecule type: mRNA
A;Residues: 2678-2729 <KAT>
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A;Residues: 1-303 cOKA>
A;Cross-references: GB:D10988; GB:D01221; NID:g221608; PIDN:BAA01761.1; PID:g221609
R;Chan, S.W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap,
J. Gen. Virol. 73, 1131-1141, 1992
A;Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship
                                                                                                                                                                                                                                                                                                                              JC5620
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001 C;Accession: A40250; P00397; P00559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;1520-1866/Product: nonstructural protein NS4a #status predicted <N4A>
;1867-2017/Product: nonstructural protein NS4b #status predicted <N4B>
;2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
;196,209,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,23
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[116.191/Product: envelope protein M #status protein 
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Taylor, L.A.; Simmonds, 6, 44-49, 1997
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Pred. No. 3.9e-05;
3; Mismatches 40
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PMID:1314459
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protein NS5
                                  P.; Elliott,
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C;Superfamily: hepatitis C virus genome
C;Keywords: glycoprotein
F;l-191/Product: core #status predicted
                                                                                                                                                     A;Title: Cloning and phylogenetic analysis of the core, A;Reference number: PC2219; MUID:94338342; PMID:7520237 A;Accession: PC2219
                                                                                                                                                                                                                                                                                          polypeptide - hepatitis C virus (type 5a) (fragments)
N;Contains: core protein; El (carboxyl end); E2/NS1 (amino end);
C;Species: hepatitis C virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
C;Accession: PC2219
                                                                  A;Molecule type: mRNA
A;Residues: 1-876 <5TU>
A;Cross-references: GB:L29577;
A;Experimental source: serum
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F:12-389/Product: major envelope protein E #status predicted <M
F:384-408/Region: hypervariable #status predicted <
F:390-730/Product: monstructural protein NS1 #status predicted <
F:731-1007/Product: nonstructural protein NS2 #status predicted <
F:7031-1008-1616/Product: hepacivirial protein NS2 #status predicted F:1008-1616/Product: hepacivirial #status predicted <NS3>
F:1231-1238/Region: nucleotide-binding motif A (P-loop)
F:1313-1318/Region: nucleotide-binding motif B
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A; Residues: 1-3014 < CHA>
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Pred. No. 0.00011;
0; Mismatches 127
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hypothetical protein - hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Nov-2000
C;Accession: S35629
R;Sarashina, T.; Sakurai, T.; Watanabe, Y.; Kashima, K.; Suzuki, T.; Chiba, J.; Kita, Y.
Nucleic Acids Res. 21, 1037, 1993
A;Title: Nucleotide sequence of the hepatitis C virus genome from a patient negative for A;Beference number: S35629; MUID:93197128; PMID:8383835
A;Accession: S35629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-125 <ARA
A;Cross-references: EMBL:D11353; NID:g221625; PIDN:BAA01956.1; PID:g221626
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
C;Superfamily: hepatitis C virus genome polyprotein
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F;339-411/Region: NS1 (amino end)
F;4312-783/Product: NS3 #status predicted <NSR>
F;412-783/Product: NS4 #status predicted <NSA>
F;784-837/Product: NS4B #status predicted <NSB>
F;838-876/Product: NS4B #status predicted <NSB>
F;838-876/Product: NS4B #status predicted <NSB>
Search completed: July 25, 2003, 13:12:47 Job time: 43 secs
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Best Local Similarity
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                                                                                                                   DKEVLYEAFDEMEECASKATLIEEGORIAEMLKSKIO 95
                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 188; DB 2; Length 125; ilarity 50.5%; Pred. No. 5e-06; Conservative 10; Mismatches 32; Indels
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Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 38, App1 Sequence 40, App1	e 40,	æ	e 60,	e 60,	e 62,	e 62,	e 200	e 200	e 270	e 270	e 198	e 198	ወ	e 16,	e 9,	Sequence 2, Appli	e 18,	e 11,	Sequence 4, Appli	w -	e 1,	æ	е ч	e 20	Sequence 20, Appl	e 20,	e 20,	Sequence 9, Appli

ALIGNMENTS

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JEONGE-NASCIEMENTO, Carlos

APPLICANT: COIT, Doris

APPLICANT: MEDINA-SELBY, Angelica

TITLE OF INVENTION: HCV ANTIGEN/ANTIBODY COMBINATION ASSAY

FILE REFERENCE: 2302-16073 / PP16073.003

CURRENT APPLICATION NUMBER: US/09/881,239

CURRENT FILING DATE: 2001-06-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 829

TYPE: PAT

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Best Local Similarity
Matches 118; Conserv
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                                                                                                                                 167 KPAIIPDREVLYREFDEMEE-SQHLPYIEQGMMLAEQFKQKALAFASRGNHVAPTHYVTE 225
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286 KEKVLAFASRGNHVSPRHYVPESEPQVVVTPDKEILYEAFDEMEE-ASKAALIEEGQRMA 344
                                  --GKPAIVPDKEVLYQQYDEMEE-
                                                     SDAKPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQF 285
                                                                                                            KPAIIPDREVLYREFDEMEECSOHLPYIEQGMMLAEQFKQKALGL-SRG-------
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                                    -CSQAAPYIEQAQVIAHQF 483
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APPLICANT: MEDINA-SELBY, Angelica
TITLE OF INVENTION: IMMUNASSAYS FOR ANTI-HCV ANTIBODIES
FILE REFERENCE: 2302-17039 / PP1703 0.02
CURRENT APPLICATION NUMBER: US/09/881,654
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/212,082
PRIOR APPLICATION NUMBER: 60/212,082
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-19
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/280,867
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                                                                                                                                                                             Sequence 2, Application US/10085476 Publication No. US20020164722A1 GENERAL INFORMATION:
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SEQ ID NO 4
LENGTH: 1099
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                     APPLICANT: De Francesco, Raffaele
APPLICANT: Tomei, Licia
APPLICANT: Tomei, Licia
APPLICANT: Behrens, Sven-Erik
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE
TITLE OF INVENTION: TRANSFERASE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HEFILE REFERENCE: IT0002PCA
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APPLICANT: ARCANGEL, Phill:
APPLICANT: TANDESKE, Laura
CURRENT APPLICATION NUMBER: US/10/085,476
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APPLICANT: COLT, Doris
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                788
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Pred. No. 1.2e-34;
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; OTHER INFORMATION: ; OTHER INFORMATION: US-10-259-275-40
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CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/171,909
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 09/747,419
PRIOR APPLICATION NUMBER: US 09/325,236
PRIOR APPLICATION NUMBER: US 60/325,236
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/338,123
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; LENGTH: 2201
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 08/952,981
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PCT/IT96/00106
PRIOR FILING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: RM95A000343
PRIOR FILING DATE: 1995-05-25
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                       SOFTWARE: Pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 40, Application US/10259275
Publication No. US20030125541A1
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TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USFILE REFERENCE: 265.0007 0120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lemon, APPLICANT: Yi, M:
                                                                                                                                                                                                PRIOR FILING DATE: 2001-11-13 NUMBER OF SEQ ID NOS: 73
                                                             TYPE: PRT
ORGANISM: ARTIFICIAL
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                ENGTH: 2985
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                    amino acid sequence encoded by nucleotides 2077-11121 of SEQ NO:39 \,
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31.1%; Pred. No. 1.1e-12;
ative 31; Mismatches 75
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Query Match Best Local Similarity

14.0%; Score 255; DB 15; 31.5%; Pred. No. 2.1e-12;

Length 2985;

Matches

Conservative

31,

Mismatches

Indels

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LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-1
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2
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TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
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86; Conserv
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                                                              GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGÁV 1913
                                                                                                                            TAAVTSPLTTGQTLLENILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILA 1853
                                                                                                                                                                                              ----ITPAV----QTNWQKLEVFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYGAGVAGALVAFKVMSGEAPSAEDLINLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1884
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                          QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                             -----IPDREVLYREFDEMEESQHL--PYIEQGMML
                                                                                                                                                             -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------
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                                                                                                                                                                                                                                                                                               14.0%; SUC. 32.2%; Pred. No. 2...
ive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                           Score 255; DB 9; Ler
Pred. No. 2.1e-12;
Pred. 77;
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US-09-238-076-2
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US-09-891-894-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09238076 Patent No. US20020102540A1
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APPLICANT: Maddon, Paul
TITLE OF INVENTION: USES OF DC-SIGN AND DC-SIGNR FOR INHIBITING HEPATITIS C VIRU
FILE REFERENCE: 2048/64896/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/891,894
CURRENT FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/238,076
                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                        ADDRESSEE: HU. 7733 F
                                                                                            FILING DATE
                                                                                                                                                                                                                                          ZIP: 63105
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                                                                                                                                                                                                                                                                                                FOUIS
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                                  US 09/034,756
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Pred. No. 2.1e-12;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: FRAGMENT TYPE:
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TOPOLOGY: lir
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REFERENCE/DOCKET NUMBER: 60
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                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                APPLICATION NUMBER: US/09/034,756
FILING DATE: 04-May-1998
ATTORNEY/ACENT INFORMATION:
NAME: HOLLAND, DONALD R.
                                                                                 PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: FUNCTIONAL
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                                                                                              APPLICATION NUMBER: US/09/995,937
FILING DATE: 28-No. US20030028010A1-2001
CLASSIFICATION: UNknown>
                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 63105
                                                                                                                                                                                                                                                                                         STATE: MO
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NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IPDREVLYREFDEMEESQHL--PYIEQGMML------
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linear
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Pred. No. 2.1e-12;
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Sequence 2, Application US/09917563 Publication No. US20030073080A1
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                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/917,563
FILING DATE: 27-Jul-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                    APPLICATION NUMBER: 09/238,076
FILING DATE: 26-JAN-1999
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS
VIRUS (HCV) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
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HYPOTHETICAL: N.O
FRAGMENT TYPE: N-Cerminal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ST. LOUIS
STATE: MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFKQKALAFASRGNHVAPTHYVTESDA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------
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STRANDEDNESS: single
  REFERENCE/DOCKET
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  NUMBER:
6029-4831
                                                                                                                                                                                                                                                               Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23, Application US/09941611 Patent No. US20020106640A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 314-727-6092 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                 ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1

CURRENT APPLICATION NUMBER: US/09/941,611

FILING DATE: 30-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAERTENS, GEERT VAN HEUVERSWUN, HUGO
TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF
                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1691 KPAIIPDREVLYQEFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: N-terminal SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86;
                                                                                                                                                                                                                                                                                                                      STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PYIEQGMML-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAVTSPLTTGQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLVDILA 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ITPAV-----QTNWQKLEVFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                        APPLICATION NUMBER: 08/391,671
FILING DATE: 1995-02-21
APPLICATION NUMBER: WO PCT/EP91/02409
                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 3012 amino acids
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POLLET, DIRK
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Pred. No. 2.1e-12;
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US-10-044-995-23
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Publication No. US2003
GENERAL INFORMATION:
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TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 23:
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/10/044,995
FILING DATE: 15-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SYNTHETIC ANTIGENS FOR THE DETECTION OF ANTIBODIES TO HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1914 QWMNRLIAFASRGNHVSPTHYVPESDA 1940
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FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DELEYS, ROBERT J
POLLET, DIRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1691 KPATIPDREVLYREFDEMEECSOHLPYTEQGMMLAEQFKQKALGLLQTASRQAEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1487-5 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1854 GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 -AQVIAHQFKEKVLAF------ASRGNHDSPTHYVPESDAKPAI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 RPAVIPDREVLYQEFDEMBEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.0%; Score 254; DB 10; Similarity 31.8%; Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLIDILA 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----IAPAV-----QTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
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                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                               STATE: VA
                                                                                                                                                                                                                                   CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SADOFF
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VAN HEUVERSWUN, HUGO
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                                                                 Version #1.30
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                NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09916359
Patent No. US20020034734A1
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                                                                                                                                          APPLICANT: Veronique Barban
TITLE OF INVENTION: VACCINE COMPOSITION FOR
TITLE OF INVENTION: TREATING C HEPATITIS
EILE REFERENCE: PMCF97-03A
CURRENT APPLICATION NUMBER: US/09/916,359
CURRENT FILING DATE: 2001-07-26
                                                                        PRIOR APPLICATION NUMBER: 09/388,874
PRIOR TLING DATE: 1999-09-02
PRIOR APPLICATION NUMBER: 97/02,887
PRIOR FILING DATE: 1997-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/920, 286
FILING DATE: 14-OCT-1992
APPLICATION NUMBER: WO PCT/EP91/02409
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: EP 90124241.2
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1794 TAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLGKVLIDILA 1853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                1914 QWMNRLIAFASRGNHVSPTHYVPESDA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1854 GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
3011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IAPAV-----QTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/391,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 2894 amino acids
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Pred. No. 2.4e-12;
""" matches 77;
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APPLICANT: Lemon, Stanley M.

APPLICANT: Yi, MinKyung

TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE

FILE REFERENCE: 265.0007 0120

CURRENT APPLICATION NUMBER: US/10/259,275

CURRENT FILING DATE: 2003-01-13

PRIOR APPLICATION NUMBER: US 60/171,909

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 09/747,419

PRIOR APPLICATION NUMBER: US 09/747,419

PRIOR APPLICATION NUMBER: US 60/335,236

PRIOR APPLICATION NUMBER: US 60/325,236

PRIOR APPLICATION NUMBER: US 60/338,123

PRIOR APPLICATION NUMBER: US 60/338,123

PRIOR FILING DATE: 2001-11-13

NUMBER OF SEQ ID NOS: 73

**COFFMANDE: DATE: 2001-11-13
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                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: amino acid sequence encoded by the nucleotides 2119-8073; OTHER INFORMATION: SEQ ID NO:41
US-10-259-275-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 42
                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
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                                                                                                                                                                                                                                                                        Query Match
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Best Local
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TYPE: PRT
ORGANISM: ARTIFICIAL
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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1914 QWMNRLIAFASRGNHVSPTHYVPESDA 1940
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                                                             721 ----AAPVVESKWRTL-----EAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMA 767
                                                                                                                                              666 KPATIPDREVLYREFDEMEECASHLPYTEQGMQLAEQFKQKATGLLQTATKQAEA-----
                                                                                                      79 VPESDARPAIIPDREVLHREFDEMEEAFASR--GNHVSPAHYVPESDASQAAPYIEQ---
                                                                                                                                                                          23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
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                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                  Score 251; DB 15;
Pred. No. 2.6e-12;
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NAME/KEY: Duplication LOCATION: 848 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Tyr or Asn" FEATURE: NAME/KEY: Duplication LOCATION: 1114 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Pro or Ser" FEATURE: NAME/KEY: Duplication LOCATION: 1176 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Pro or Thr" NAME/KEY: Duplication LOCATION: 1276 LOCATION: 1344 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Pro or Leu" FEATURE: NAME/KEY: Duplication LOCATION: 1454 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Cys or Tyr" NAME/KEY: Duplication LOCATION: 1979 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Glu or Gly" FEATURE: NAME/KEY: Duplication LOCATION: 1949 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Leu or His" LOCATION: 1949 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Ser or Cys" FEATURE: NAME/KEY: Duplication LOCATION: 1949 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Gly or Val" LOCATION: 2021 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Gly or Val" NAME/KEY: Duplication LOCATION: 2021 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Gly or Val" NAME/KEY: Duplication LOCATION: 2021 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Thr or Ser" NAME/KEY: Duplication LOCATION: 2021 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Thr or Ser" NAME/KEY: Duplication LOCATION: 2021 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Thr or Ser" NAME/KEY: Duplication LOCATION: 2021 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Thr or Ser" NAME/KEY: Duplication LOCATION: Duplication L	SCHENCE 64.3-6 SCHENERAL INCOMPATION. GENERAL INCOMPATION. GENERAL INCOMPATION. TITLE OF INVESTIGATE HAVE AND INFROVED SOLUBILITY CORRESPONDENCE ADDRESS. APPLICANT: HOGHTON, MICHAEL CHON, JUL LIM NUMBER OF SEQUENCES. HELICASE ACTIVITY AND INFROVED SOLUBILITY CORRESPONDENCE ADDRESS. ADDRESSEE: CHILDRO CORPORATION STREET: Intellectual Property - R440, P.O. Box 8097 CITY. Emeryville STATE: California ACOMPTRY: U. S.A. COMPTRY: U. S.A. APPLICATION UNDER: U. S.A. APPLIC
heterogeneity at this position - Xaa = Met or Val" FEATURE: NAME/KEY: Duplication LOCATION: 603 OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Leu or Ile"	201 EQFKQKALAFASRGNHVAPTHYVTESDA 228 : ::
at this position - Xaa = Ile or plication There exists a	768 FTASITSPLTTQHTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDIL 827 171

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                                                                                                                                                                                                                                                              Sequence 20, Application US/09238076
Patent No. US20020102540A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 82; Conserv
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM For Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL D
TITLE OF INVENTION: VIRUS (HCV)
                                                                                             COUNTRY: US
ZIP: 63105
                                                                                                                                                      ADDRESSEE: HOWELL & HAFERKAMP, L.C. STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                         STREET:
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OTHER INFORMATION: /note= "There exists a heterogeneity at this position - Xaa = Leu or SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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OTHER INFORMATION:
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Pred. No. 4.6e-12;
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Search completed: July 25,

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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HOLLAND, DONAI REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
 1914
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                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                          Similarity
QWMNRLIAFASRGNHVSPTHYVPESDA 1940
                                                              GYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                    QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                            -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                            -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI-----
                                                                                                                                                                                             ----ITPAV-----QTNWQKLEVFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3011 amino acids
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                                                                                                                                                                                                                                                                                                                        Score 250; DB 10;
Pred. No. 5.6e-12;
6; Mismatches 78;
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Gaps

78 10;

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Result
No.
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ORIGINAL SOURCE:
ORGANISM: Hep:
US-08-921-887-52
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GENERAL INFORMATION:
Best Local Similarity Matches 352; Conserv
                                             Query Match
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Patent No. 6030771
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                             STRANDEDNESS:
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ALIGNMENTS	US-09-315-850-14 US-08-811-566-2 US-09-034-756-2 US-08-850-328-4 US-08-444-818-30 US-08-444-818-66 US-08-444-818-69 US-08-444-818-23 US-08-466-975A-23 US-08-466-975A-23 US-08-461-92A-23 US-08-475-265-23 US-08-475-265-23 US-08-440-11-23 US-08-440-11-23 US-08-440-103-36 US-08-440-519-10 US-08-440-519-10 US-08-440-519-10 US-08-231-368-36
	Sequence 14, Appl Sequence 2, Appli Sequence 2, Appli Sequence 30, Appli Sequence 66, Appli Sequence 66, Appl Sequence 23, Appl Sequence 13, Appl Sequence 136, Appl Sequence 136, Appl Sequence 136, Appl Sequence 10, Appl

CORRESPONDENCE ADDRESS: ADDRESSEE: JONES & ASKEW, LLP STREET: 191 Peachtree Street, APPLICANT: KHUDYAKOV, YURI E. APPLICANT: FIELDS, HOWARD A. TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION TITLE OF INVENTION: ENDONUCLEASE ASSISTED LIGATION NUMBER OF SEQUENCES: 55 N.W. 37th Floor METHOD FOR MAKING THE SAME

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/921,887
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WARREN, WILLIAM L.
REGISTRATION NUMBER: 03063-0380
TELECHOME: 404-818-3700
TELEPHONE: 404-818-3700 Version

SEQUENCE CHARACTERISTICS: LENGTH: 352 amino acids TYPE: amino acid NO VPE: internal not relevant Hepatitis virus not relevant

Conservative 100.0%; Score 1818; DB 100.0%; Pred. No. 7.6e-1 0, Mismatches DB 3; Length 352; Indels 0, Gaps

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                                      Query Match
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Patent No. 5610009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MAMMALIAN EXPRESS
TITLE OF INVENTION: ENVELOPE GENES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D3:
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                 TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/188,281B
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                       Local
                                                                                                                                          TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDEMEESQHLPYIEQGMMLAEQFKQKALAFASRGNHVAPTHYVTESDAKPALVPDKEVLY 240
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DEVARE, SUSHIL G.
VENTION: MAMMALIAN EXPRESSION
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14.1%; Score 257; DB 1; 32.5%; Pred. No. 7.4e-15; tive 27; Mismatches 74
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                                  Length 3011;
Indels
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 80;
Gaps
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US-08-453-552-1
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Query Match
Best Local Similarity
Matches 87; Conserv
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Patent No. !
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,552
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
                                                                                                                                                                              TELEPHONE: 708-937-636
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FRAMAGUCHI, JULIE
APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
APPLICANT: DESAI, SURSHIL G.
TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 12
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                                                                                                                      TYPE: amino a STRANDEDNESS:
                                                                                                             TOPOLOGY:
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                                                                                                           ss: single
linear
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14.1%; Score 257; DB 1; Length 3011; 32.5%; Pred. No. 7.4e-15; tive 27; Mismatches 74; Indels 8
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Conservative

90;

Gaps

; MOLECULE TYPE: protein US-08-710-637-1	MECATION INFORM ME: 708-937-6; 1: 708-937-95; 1: 708-937-95; 1: FOR SEQ ID NO CHARACTERISTIC: 3011 amino ac amino acid DNESS: single EDNESS: single	OR APPLICATION DATA: PPLICATION NUMBER: US/08 ILING DATE: PPLICATION NUMBER: US 07 ILING DATE: 01-JAN-1992 ILING DATE: 11-JAN-1992 ORNEY/AGENT INFORMATION: AME: POREMBSKI, PRISCILL EGISTRATION NUMBER: 33,2	COUNTRY: USA ZIP: 60064-3500 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/710,637 FILING DATE: CLASSIFICATION: 435	ILE CENT	pplicati 54001 RMATION: CASEY, BODE, ZECK, YAMAGU	Qy 201 EQFKQKALAFASRGNHVAPTHYVTESDA 228 : :	Qy 171A 200 Oy 171A 200 B 1853 AGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA 1912	QY 134AQVIAHQFKEKVLAFASRGNHDSPTHYVPESDAKPAI 170	Qy 23 RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAFASRQNHVSPTHY 78	
Query Match 14.1%; Score 257; DB 5; Length 3011; Best Local Similarity 32.5%; Pred. No. 7.4e-15;	TELEPHONE: 708-937-856 TELEPAK: 708-937-9556 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3011 amino acids TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein PCT-US93-00907-1	APPLICATION NUMBER: PCT/US93/00907 FILING DATE: 19930129 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: PORRMSKI, PRISCILLA E. REGISTRATION NUMBER: 33,207 REFERENCE/DOCKET NUMBER: 5111.PC.01 TELECOMMUNICATION INFORMATION:	STREET: ONE ABBOTT PARK ROAD CITY: ABBOTT PARK STATE: IL COUNTRY: USA 2IP: 60064-3500 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	APPLICANT: ZECK, BILLY J. APPLICANT: YAMAGUCHI, JULIE APPLICANT: DESAI, DONALD E. APPLICANT: DESAI, SURESH M. APPLICANT: DESAI, SURESH M. APPLICANT: DEVARE, SUSHIL G. TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HCV TITLE OF INVENTION: PROTEINS INTHER OF SEQUENCES: 12 CORRESPONDENCE ADBRESS: ADDRESSEE: ABBOTT LABORATORIES D377/AP6D	200 Β ΩΩ	Qy 171A 200 Qy	Qy 134AQVIAHQFKEKVLAFASRGNHDSPTHYVPESDAKPAI 170	Qy 79 VPESDARPAIIPDREVLHREFDEMEEAFASRGNHVSPAHYVPESDASOAAPYIEQ 133	Query Match 14.1%; Score 257; DB 2; Length 3011; Best Local Similarity 32.5%; Pred. No. 7.4e-15; Matches 87; Conservative 27; Mismatches 74; Indels 80; Gaps 10; Matches 87; Conservative 27; Mismatches 74; Indels 80; Gaps 10; Qy 23 RPAVIDDREVLYQEFDEMEEAS-HLPYIEQGMOLAEQFKQKALAFASRQNHVSPTHY 78 Qy 23 RPAVIDDREVLYQEFDEMEECSQHLPYIEQGMMLAEQFKQEALGLLQTASRQAEV 1745	

Matches

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Mismatches

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Best Local Similarity
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                                                                                                                                                                                                                                           TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino aci
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 55
TELECOMMUNICATION INFORMATION: 708-937-6365
                                                                                                                                               TOPOLOGY: li
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ATTORNEY/AGENT IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WATANABE, SHINICHI APPLICANT: YAMAGUCHI, JULIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521 US.01
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1793
1691 KPATIPDREVLYQEFDEMEECSQHLPYTEQGMMLAEQFKQEALGLLQTASRQAEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1853 AGYGAGVAGALVAFKIMSGEVPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA 1912
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                  RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
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                                                                                                                                                                                                             3011 amino acids
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DEVARE, SUSHIL G.
VENTION: MAMMALIAN EXPRESSION SYSTEMS FOR
                                                                 Conservative
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DESAI, SURESH M.
                                                                                                                                                               linear
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                                                          Score 257; DB 5, -
Pred. No. 7.4e-15;
***:ematches 74;
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                                                                                          Length 3011;
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PCT-US95-01087-1
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5521.US.01
                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                       CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                           79 VPESDARPAIIPDREVLHREFDEMEEAFASR--GNHVSPAHYVPESDASQAAPYIEQ--- 133
                                                                                                                                           87;
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                                                                                                                                                                                                                                                                                       3011 amino acids
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                                                                                                                                                                                                                                                                                                                                    708-938-2623
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             ---ITPAVQTNWQKL------EAFWAKHMWNFISGTQYLAGLSTLPGNPAIASLMA 1792
                                                                                                                                           Conservative
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DESAI, SURESH M.
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                                                                                                                                        27;
                                                                                                                                                         Score 257; DB 5;
Pred. No. 7.4e-15;
                                                                                                                                          Mismatches
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US-08-324-977-12
                                                      NFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
PRIOR DATE: 28-DEC-1990
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
               SEQUENCE CHARACTERISTICS LENGTH: 2013 amino aci
                                                                                                          TELEPHONE: (202) 659-2930
                                                                                                                                                                                                  FILING DATE: 28-DEC-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
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                                                                                                                                            NAME: Stevens-Smith, Theresa M. REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-JU
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                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/099,706 FILING DATE: 30-JUL-1993
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1725 K St. N.W. Suite 1000
               2013 amino acids
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MORI, Chisato
                                                                                      (202) 887-0357
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                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/
FILING DATE: 02-0CT-1991
APPLICATION NUMBER: UP 2-1
FILING DATE: 25-UN-1990
PRIOR APPLICATION NUMBER: UP 2-2
APPLICATION NUMBER: UP 2-2
FILING DATE: 31-AUG-1990
PRIOR APPLICATION NUMBER: UP 2-3
APPLICATION NUMBER: UP 2-3
                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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                                FILING DATE: 09-NOV-
PRIOR APPLICATION DATA:
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CLASSIFICATION:
APPLICATION NUMBER: US 07/635,451 FILING DATE: 28-DEC-1990
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MORI, Chisato
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31.1%; Pred. No. 5.1e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08904686A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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           APPLICATION NUMBER: US/08/904,686A FILING DATE: 01-AUG-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/324,977
                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
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LENGTH: 2013 amino acids
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                                                                                                                                                                                                                              STATE: D.C.
                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                             STREET:
 APPLICATION NUMBER: 18-OC
                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                            COMPUTER:
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                              ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
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REFERENCE/DOCKET NUMBER: 900703
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1725 K St. N.W. Suite 1000
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MORI, Chisaco
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                                                                                                                                        IBM PC compatible
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18-OCT-1994
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Pred. No. 5.1e-15;
1; Mismatches 75;
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RESULT 11
US-09-315-850-12
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Best Local Similarity
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                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman,
ADDRESSEE: Naughton
                                                              APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 2013 amino aci
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
                                                       UMBER OF SEQUENCES:
                                                                                                                         APPLICANT:
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                                                                                                                                    FUKE, Isao
MORI, Chisato
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                     Hattori,
                   McLeland
                                                                                     GENOMIC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                J-315-850-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: MCLeland, Le-Nhung
REGISTRATION UMBER: 31,541
REFERENCE/DOCUMENT: 31,541
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1i MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
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PRIOR APPLICATION DATA:
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CITY: Washington
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IOR APPLICATION DATA:
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OFKOKALAFASRGNHVAPTHYVTESDA
                                GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                                 +AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI-----
                                                                                               TÄSITSPLTTQSTĹLÉNILGGWVAÄQLAPPSAASAFVGAGIÁGAÄVGSIGLGKVLVDILA 1853
                                                              -----IPDREVLYREFDEMEESQHL--PYIEQGMML-------AE 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS, Version
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                                                                                                                                                                                                                                                                                                                  14.1%; Score 256; DB 3; 31.1%; Pred. No. 5.1e-15;
                                                                                                                                                                  ----VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
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RESULT 13
US-08-324-977-32
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US-08-952-981A-2
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SEQ ID NO 2
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CURRENT APPLICATION NUMBER: US/08/952,981A
CURRENT FILING DATE: 1998-03-23
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 2201
                                                                                                                                              TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS TITLE OF INVENTION: CDMA AND ANTIGEN POLYPEPTIDE NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
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                                                 COUNTRY:
                                                                                                               ADDRESSEE:
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                                                                              Washington
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                                                                  D.C
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1725 K St. !
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                                                 U.S.A.
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                                                                                                                               Armstrong, Westerman, Hattori, McLeland
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RESULT 14
US-08-384-616+32
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                                                        Sequence 32, Appli
Patent No. 5847101
GENERAL INFORMAT!
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                                                                                             Application US/08384616
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 MORI, Chisato
                                       OKAYAMA, Hiroto
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30-JUL-1993
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31.1%; Pred. No. 7.5e-15;
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// MOLECULE TYPE: protein
US-08-384~616-32
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 2-
FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US (FILING DATE: 02-OCT-1991)
APPLICATION NUMBER: JP
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Armstrong, Westerman, Hattori, McLeland
ADDRESSEE: Naughton
                                                                                                                                                                                                                                                              1302 RPAIVPDRELLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                                                                                                                  134
202 QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                     79 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                                                                                                                                                                                               23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
                                                                                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20006
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                                     GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                             TASITSPLTTQSTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA 1464
                                                                                                                                                -AQVIAHQFKEKVLAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stevens-Smith, Theresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVENTION: CDNA AND ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION:
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                                                                        -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202)
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                                                                                                                                                                                                                                                                                                                                                        14.1%;
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                                                                                                                                                                                      ----VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1404
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                                                                                                                                                                                                                                                                                                                                   Score 256; DB 2;
Pred. No. 7.5e-15;
1; Mismatches 75;
                                                                                                                                                - ASRGNHDSPTHYVPESDAKPAI -
                                                                                                                                                                                                                                                                                                                                                                      Length 2620;
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78;

AE

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1525 QWMNRLIAFASRGNHVSPTHYVPESDA 1551

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US-08-904-686A-32
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US-08-904-686A-32
 Query Match 14.1%; Score 256; DB 2; I Best Local Similarity 31.1%; Pred. No. 7.5e-15; Matches 83; Conservative 31; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/08904686A
                                                                                                                                                                                        TELEPHONE: (202) 659-2
TELEFAX: (202) 887-035
(NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENERAL INFORMATION:
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                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2620 amino aci
                                                                                                                                                                                                                                                    NAME: MCLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/904,686A FILING DATE: 01-AUG-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 31-AUG-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 25-JUN-PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/099,706 FILING DATE: 30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 09-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 18-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1725 K St
CITY: Washington
STATE: D.C.
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                                                                                                                                     amino acid
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TAKAMIZAWA, Akahisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                  (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: JP 2-305605
09-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: JP 2-167466
25-JUN-1990
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31-AUG-1990
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1525 QWMNRLIAFASRGNHVSPTHYVPESDA 1551
                                                                                                       171
                                                                                                                                                                            134 -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------ 170
                               202 QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                                                VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                                                                                                                 ----AAP-----VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1404
                                                                                                       -----IPDREVLYREFDEMEESQHL--PYIEQGMML--
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Search completed: July 25, 2003, 13:13:24 Job time : 32 secs

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Minimum DB
Maximum DB
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Perfect score:
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length: 2000000000
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Match
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1818
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(without alignments)
657.315 Million cell updates/sec
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.: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:
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                   AAY06672
AAE18690
AAU76378
ABG72262
AAR30616
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AAR68864
                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                          chance to have a result being printed,
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                 Amino acid sequence Multiple epitope fi HCV multiple epito HCV multiple epito Polypeptide coded Partial HCV non-st Encoded by full-le Hepatitis C virus
                                                                                                                                                                                                      Description
Protein sequence
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0 0 0 0 0 0 0 0 0 0 4 4 4 4 4 4 4 4 4 4	44444444444444444444444444444444444444	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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Hepatitis C virus Hepatitis C virus Peptide encoded by Sequence encoded i HCV polypeptide 1. Sequence encoded i Peptide encoded by	quence enc V NS35 pol V delNS35 ino acid s ino acid s ino acid s ino acid s ino acid s	on-B vira on-B vira on-B hepa on-B repa on-B repa on-B repa on-B repa on-B repa on-B repa on-B virus on-B viru	PT-NANBH virus non HCV antigen T7N1-3 Hepatitis C virus Portion of PT-NANB Blood transmiscibl HCV protein cleava HCV genomic amino HCV sequence. Hep HCV NS2-NS5B non-s

ALIGNMENTS

RESULT 1
AAY06672
ID AAY

AAY06672 standard; Protein; 352 AA.

17-JUN-1999 AAY06672;

(first entry)

Amino acid

sequence of the NS4 mosaic protein.

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New mosaic protein, comprising a plurality of homologous antigenic peptides from different genotypes of a species - useful for
                                                                                                                                                                    Hepatitis C virus. Synthetic.
                                                                                        25-AUG-1997;
                                                                                                                                                                                                 Mosaic protein; antigenic peptide; nucleocapsid; NC; hepatitis; REAL; restriction endonuclease assisted ligation; vaccination; NS4 antigen.
                              WPI; 1999-204671/17
                                                Fields HA,
                                                                                                           21-AUG-1998;
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                                                                                                                                                  WO9910506-A1
                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                Khudyakov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a mosaic protein, comprising a plurality of homologous antigenic peptides from different genotypes of a species. The antigenic peptides are from nucleocapsid (NC) porteins. A method for synthesising an artificial gene that encodes the mosaic protein is also provided. The method is designated restriction endonuclease assisted ligation (REAL). The mosaic protein and the artificial mosaic protein are useful for detecting a hepatitis infection in an individual. The mosaic gene and protein is also useful for vaccination against infection, especially hepatitis C. The method of synthesizing the artificial gene and the resulting mosaic protein improve the sensitivity, spectrum of immunoreactivity, and antigen specificity of enzyme immunoassays. This provides improved detection of hepatitis C virus. The present sequence represents the amino acid sequence of the NS4 mosaic protein.
                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; NS3/4a antigen; multiple epitope fusion antigen; HCV infection; MEFA 12 protein.
                                                                                                                                                                                                                                                                                                                                                                                                               Multiple epitope fusion antigen
        20-DEC-2001
                                                                                                                                          Misc-difference
                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE18690 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQFKEKVLAFASRGNHVS
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                                                                                                              "Encoded by
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Pred. No. 1.8e-148;
                                                                                                                                                                                                                                                                                                                                                                                                               (MEFA) 12 protein
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Best Local Similarity
Matches 118; Conserv
                                                Hepatitis C virus.
Synthetic.
                                                                                                        Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion; immunoassay solid support; multiple epitope fusion antigen; MEFA;
                                                                                                                                                                           08-MAY-2002
                                                                                                                                                                                                                                AAU76378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to hepatitis C virus (HCV) core antigen and NS (nonstructural) 3/4a antibody combination assay that can detect both HCV antigens and antibodies present in a sample using a single solid matrix as well as immunoassay solid supports for use in the assay The solid support is useful for detecting HCV infection in a biological sample. The present sequence is MEFA (multiple epitope fusion antigen) 12 protein. This sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoassay solid support useful for detecting hepatitis C virus infection in a biological sample, comprises at least one of HCV anti-core antibody and HCV NS3/4a epitope, bound to the support
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2000; 2000US-212082P
02-APR-2001; 2001US-280811P
02-APR-2001; 2001US-280867P
                                                                                          non-structural protein.
                                                                                                                                             HCV multiple epitope fusion antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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N-PSDB; AAD29796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention
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                                                                                                                                                                                                                                standard; Protein; 1099
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                                                                                                                                                                                                                                                                                                                                                                        KEKVLAFASRGNHVSPRHYVPESEPQVVVTPDKEILYEAFDEMEE-ASKAALIEEGQRMA 344
                                                                                                                                                                                                                                                                                                   EMLKSKIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPAIIPDREVLYREFDEMEECSQHLPYIEQGMMLAEQFKQKALGL-SRG-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               829 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.
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Pred. No. 1.9e-35;
6; Mismatches 15
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                                                                                                       epitope
                                                                                                                                                (MEFA) 7.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
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                                                                                                                                             protein sequence
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WO200196870-A2

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amino HCV-1 E1" acids

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of HCV-1

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RESULT 4
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AC ABG7
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O6-N
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 118
                                                                                                                                                                                                                                                                                                                                                                                                                             personal contact. Use of NS3/4a conformational epitope in combination with MEFA, provides a sensitive and reliable method for detecting early HCV seroconversion. Use of MEFA has the added advantages of decreasing masking problems, improving sensitivity in detecting antibodies by allowing a greater number of epitopes on a unit surface area of substrate, and improving substrate. Detection accuracy is increased and the incidence of false results is reduced because of the identification and the use of highly immunogenic HCV antigens which are present during the early stages of HCV seroconversion. The present amino acid sequence represents the multiple epitope fusion antigen (MEFA) 7.1 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic and prognostic tool to provide adequate patient care and to prevent transmission of HCV by blood and by blood products, or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new immunoassay solid supportions is the present ally of at least one hepatitis C virus (HCV) conformational epitope and a multiple epitope fusion antigen (1) bound to the support. The NS3/4a conformational epitope and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2000; 2000US-212082P
02-APR-2001; 2001US-280811P
02-APR-2001; 2001US-280867P
 06-MAR-2003
                                                   ABG72262
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is useful for detecting hepatitis C virus infection in a biological sample. The method of the invention provides a sensitive, accurate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEFA reacts specifically with anti-HCV antibodies present in a biological sample from an HCV-infected individual. The immunoassay of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoassay solid support, useful for detecting hepatitis C virus infection in biological sample, comprises HCV NS3/4a conformation epitope and multiple epitope fusion antigen bound to the support
                          ABG72262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                     EMLKSKIQ 352
                                                                                                                                                                                                                                         SDAKPALVPDKEVLYQQYDEMEEAFASRGNHVAPTHYVVESDASASLPYMDETRAIAGQF
                                                                                                                                                                                                                                                                              KPAIIPDREVLYREFDEMEE-SQHLPYIEQGMMLAEQFKQKALAFASRGNHVAPTHYVTE
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                                                     standard;
                                                                                                                      EMLKSKIQ
                                                                                                                                                                        KEKVLGLI - - - - :
                                                                                                                                                                                                  KEKVLAFASRGNHVSPRHYVPESEPQVVVTPDKEILYEAFDEMEE-ASKAALIEEGQRMA
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                                                                                                                      841
                                                     Protein;
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                                                   1099
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Pred. No. 2.8e-35;
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(HCV) NS3/4a
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 15-JUN-2000;
02-APR-2001;
                         (CHIE/)
(ARCA/)
(TAND/)
(GEOR/)
(COIT/)
                                                                                                                                                          14-JUN-2001; 2001US-0881654.
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Chimeric - Hepatitis C virus
Chimeric - Hepatitis C virus
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                                                                                                       02-APR-2001;
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                       CHIEN D Y.

ARCANGEL P.

TANDESKE L.

GEORGE-NASCIMENTO (
COIT D.
            MEDINA-SELBY
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2001US-280811P.
2001US-280867P.
                                                , r.
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NS5 region"
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HCV-1 E2 HVR"
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67-84 of HCV-2"
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enic determinants 64-88 of HCV-1

of HCV-1

of HCV-1

of HCV-1

of HCV-2

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AC AAR3
DT 25-M
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EW KHCV
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             10-JUN-1992;
                                                                        EP521318-A2
                                                                                                                                                                                                                                                                  AAR30616 standard; Protein; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to immunoassays comprising Hepatitis Virus (HCV) NSJ/4a conformational epitope and multiple epitope fusi antigen (MEFA), bound to a solid support. The NSJ/4a epitope and/or the multiple epitope fusion antigen react with anti-HCV antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biological samples, comprises Hepati
and multiple epitope fusion antigen
                                                                                                                              KHCV-LBC1; diagnosis;
                                                                                                                                                             Polypeptide
                                                                                                                                                                                         25-MAR-2003
19-MAY-1993
                                                                                                                                                                                                                                      AAR30616;
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                                                                                                  Korean hepatitis
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Medina-Selby A;
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(first entry)
             92EP-0109753.
                                                                                                    C virus
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Pred. No. 2.8e-35;
6; Mismatches 15
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Best Local S
Matches 102
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                            Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA and polypeptide(s) from a new type of hepatitis C virus - for diagnosing and vaccinating against KHCV infections
                                                                           proteinase;
                                                                                                        Partial HCV
                                                                                                                                       14-NOV-1996
                                                                                                                                                                     AAR82694;
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06-AUG-1991;
                                                           identification;
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Yang JY;
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                                                                                                                                                                                                                                                                                                      QFKEKVLAFASRGNHVSPRHYVPESEPQVVVT 315
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                                                                        hepatitis C virus; screening;
                                Virus.
                                                                                                       non-structural polyprotein.
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                                                         cleavage.
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91KR-0013601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 268; DB 14;
Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ST,
                                                                                                                                                                                                                                                                                                                                                                       ----NHVAPTHYVVESDASASLPYMDETRAIAG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SITSPL-------TTQHTLLFNILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ϋ́B,
                                                                           inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                          proteolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PALVPDKEVLYQQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park YW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                          1913
                                                                                                                                                                                                                                                                                                                                                                                                    1872
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Location/Qualifiers

TANK PARKET PROCESS OF THE TERMS OF THE TERM

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RESULT 7

AAR34468
ID. AAR3
XX
AC AAR3
XX
XX
DT 30-J
XX
KW HCV;
KW PO1y
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a partial Hepatitis C Virus (HCV) polyprotein from the non-structral region. Partial proteinase sequences (AAR82692-93) are contained within this sequence. The proteinases can be used as anti-HCV agents. They can also be used to screen cpds. for their ability to inhibit their proteolytic activity. In this way proteinase inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-1992;
07-FEB-1992;
18-SEP-1992;
HCV; non-A, polymerase
                                      Encoded by full-length Hepatitis C virus clone
                                                                  30-JUL-1993
                                                                                            AAR34468;
                                                                                                                     AAR34468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An HCV proteinase active substance - which has activity as an anti-HCV agent and can be used to screen for proteinase inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-287962/38.
N-PSDB; AAT03960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP07184648-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KAEN/) KAENNO K.
(SOYA-) SOYAKU GIJUTSU
(SUMQ) SUMITOMO METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be identified.
                                                                                                                                                                                                                                                                                                                                                1751
                                                                                                                                                                                                                                                                                             1800
                                                                                                                                                                                                                                          1855
                                                                                                                                                                                      1901
                                                                                                                                                                                                                                                                                                                                                                                                      1691
                                                                                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                      115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF----ASRQ------
                                                                                                                                                                                     ILRRHVGPGEGAVOWMNRLIAFASRGNHVSPTHYVPESDA
                                                                                                                                                                                                                                                                                                                                                                                                   RPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEAAAPVV
                                                                                                                                                                                                                                                                   ASRGNHDSPTHYVPESDAKPAIIPDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                                                                                                                                                            PLTTQNTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVH-----ILAG
                                                                                                                                                                                                                                                                                                                                                ESKWRALEVFWAKHMWNFISGIQYL----AGLSTLPGNPAI-----ASLMAFTASITS
                                                                                                                                                                                                                                                                                                                                                                          -----NHVSPTHYVPESDARPAIIPDREVLHREFDEMEEAFASRGNHVS
, non-B hepatitis virus; NANBHV; l chain reaction; diagnostic method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3010 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 39-48; 52pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92JP-0325303
92JP-0022657
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/note= "partial proteinase;
992..1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                     Protein;
                                                                 entry)
                                                                                                                                                                                                    14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "partial
                                                                                                                                                                                                                                                                                                                      -AHYVPESDAS------QAAPYIEQAQVIAHQFKEKVLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                     3011
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 263; DB 16;
Pred. No. 3.6e-13;
Pred. Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteinase;
                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     즛
                                                                                                                                                                                                                                        KVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAA
             liver disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3010;
                                                                                                                                                                                      1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                      148
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AAR68864
ID AAR6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA was prepared from HCV genomic RNA. Full-length clone and 14 shorter clones were isolated by PCR amplification. Primer/probes derived from the sequences of these clones c in diagnostic assays for HCV. See also AAQ40425-Q40439.
                       Hepatitis C virus
                                                 Hepatitis C virus; baculovirus; recomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 6-18; 44pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-130638/16.
N-PSDB; AAQ40426.
                                                                                        Hepatitis C virus RNA helicase
                                                                                                                  06-DEC-1995
                                                                                                                                             AAR68864;
                                                                                                                                                                       AAR68864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA and cDNA of hepatitis C virus - useful as probes diagnosing HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP05068562-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                        --AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI------
                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPAIIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTASKQAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
                                                                                                                                                                                                                                                      EQFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                                                                                                                                               FTASITSPLTTQHTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDIL 1852
                                                                                                                                                                                                                                                                                                                                                                                                                           VPESDARPAIIPDREVLHREFDEMEEAFASR--GNHVSPAHYVPESDASQAAPYIEQ---
                                                                                                                                                                                                                                        VQWMNRLIAFASRGNHVSPTHYVPESDA
                                                                                                                                                                                                                                                                                            AGYGAGVAGALVAFKGMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGA 1912
                                                                                                                                                                                                                                                                                                                                                                                                   ---- AAPVVESKWQAL----
                                                                                                                                                                                                                                                                                                                    3011 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                virus; HCV; non-A non-B; recombinant production
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-0153736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 2414
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "not defined'
                                                                                                                                                                       Protein; 3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 263; DB 14;
Pred. No. 3.6e-13;
7; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဗ
                                                                                                                                                                       B
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                                                               helicase
                                                                                                                                                                                                                                        1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74;
                                                              gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                 RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                 helicase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be
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80;

Gaps

78 11;

170

200

133

used

В δ 멍 Ş D В á В Ś

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Query Match
Best Local S
Matches 86
                                                         AAQ81559 encodes AAR68864 hepatitis C virus (HCV) RNA helicase. DNA was used in the construction of an expression vector, which was used to transform a baculovirus host. The transformed baculovirus could then be used for the recombinant prodn. of
                                   Sequence
                                                                                                      Claim 1;
                                                                                                                      Expression of hepatitis C virus helicase gene in baculovirus useful for large scale prodn. of RNA helicase.
                                                                                                                                                                                           18-SEP-1992;
                                                                                                                                                                                                            18-SEP-1992;
                                                                                                                                                                                                                              22-NOV-1994
                                                                                                                                                                                                                                               JP06319583-A
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                                                                                                                                                                          (SOYA-) SOYAKU GIJUTSU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                    RNA helicase.
                                                                                                                                                 1995-040330/06.
DB; AAQ81559.
  96;
          Similarity
                                                                                                    Fig 1-4; 9pp; Japanese
                                   3010 AA
  Conservative
                                                                                                                                                                                           92JP-0249241
                                                                                                                                                                                                            92JP-0249241
                                                                                                                                                                                                                                                                                                           /label= N-linked
2077..2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448..450
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/label= N-linked glycosylation
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         14.3%;
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                                                                                                                                                                                                                                                                                                                                   N-linked
 28;
Score 260; DB 16;
Pred. No. 6.4e-13;
8; Mismatches 75;
                                                                                                                                                                                                                                                                                glycosylation site
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                Length 3010;
 Indels
78;
Gaps
                                                                                     The
10;
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RESULT 9
AAP90158
ID AAP9
XX AAP9
XX AAP9
XX AAP9
XX 10-N
XX POOL
XX POOL
XX POOL
XX POOL
XX PAN
XX 18-N
PR 26-G
PR 26-G
XX PR 30-G
PR 26-G
XX HOUG
XX HOUG
XX HOUG
XX PT HEPB
PT Of 1
XX PT Of 1
XX Disc
CC The
CCC (NAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1987;
30-DEC-1987;
26-FEB-1988;
26-OCT-1988;
                                             The sequence is encoded by the composite cDNA of AAN90327. Thes antigens react with antibodies in patients with non-A non-B hepa (NANBH). They can be used to diagnose HCV-induced MANBH, to rais antibodies for immunoassay or treatment, or to produce vaccines. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                             Hepatitis C virus gene - used for prodn. of polynucleotide polypeptide(s) and antibodies for diagnosis, prevention and of infection.
     Sequence
                                                                                                                                                                                                                                                                                                                                                WPI; 1989-215054/30
N-PSDB; AAN90327.
                                                                                                                                                                                            Disclosure; fig 26; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB2212511-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein sequence of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
10-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP90158 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP90158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIRON CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                     Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IPDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TASITSPLTTONTLLENILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
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     1786 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                     Choo QL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0122714.
87US-0139886.
88US-0161072.
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raise
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d treatment
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23

RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY

Query Match Best Local S Matches 84

Similarity

14.2%;

Conservative

28;

Score 259; DB 10; Pred. No. 3.8e-13; 3; Mismatches 77;

Length:

78;

Gaps

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                        The NS4 region from the 3' region of the PT-NANBH genome (AAQ46195) is amplified by PCR using primers D224 and D226 (AAQ46196-97) and the fragment (AAQ46198) is cloned into a vector and expressed in infected insect cells. The recombinant virus (BHC-19) was able to express the NS4 specific recombinant virus (BHC-19) was able to express the NS4 specific recombinant protein at low levels in the infected insect cells.

If at least three different PT-NANBH antigens are used to screen for PT-NANBH, the screening is much more sensitive as compared to the use of only two PT-NANBH antigens. Pref. antigens are described in AAQ46192-94. Two new antigenic regions of the PT-NANBH genome are given in AAQ46198-99. AAQ46202 describes an improved PT-NANBH recombinant polypeptide.

(Updated on 25-MAR-2003 to correct PN field.)
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A41435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parenterally transmitted non A non B hepatitis; PT-NANBH; NS4; hepatitis C virus; HCV; detection; diagnosis; antigen; vaccine; amplification; primer; polymerase chain reaction; PCR.
                                                                                                                                                                                                                                                                                 New recombinant polypeptide for diagnosing hepatitis {\tt C} - contains three distinct antigens from different viral regions, also useful in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR41435 standard; Protein; 2354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parenterally transmitted non
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT-NANBH virus non-structural proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003 (updated)
24-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR41435;
                                                                                                                                                                                                                                                     Example 1; Page 43-53; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Parker D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9317110-A2
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 (WELL ) WELLCOME FOUND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1198
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                                                                                                                                                                                                                                                                                                                                                                    1993-288415/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWMNRLIAFASRGNHVSPTHYVPESDA 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYGAGVAGALVAFKIMSGÉVPSTÉDLVNÍLPAILSPGALVVGVVCAAILRRHVGPGEGÁV 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AQVIAHQFKEKVLAF----
                                                                                                                                                                                                                                                                                                                                                                                                  Rodgers BC
2354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               92GB-0003803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93WO-GB00345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ARAVHTNWQKLETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A non B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ASRGNHDSPTHYVPESDAKPAI-----
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RESULT 11
AAR29527
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Best Local S
Matches 86
                                                                                                                                                        11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                                                                                                                                                                                                                                                                                                                                                Clone; Hepatitis C Virus; HCV; core-envelope; NS1(gp70) NS4-NS5; region; diagnostic method; antibody; supress; proteolytic; process; precursor; polypeptide.
                                                                                    WPI;
                                                                                                      Hayashi N,
Teranishi Y;
                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                          HCV antigen T7N1-30
                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR29527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR29527 standard;
                    Claim 1 and 3; Page 259-272; 305pp; English.
                                         New hepatitis C virus gene diagnosing and vaccinating
                                                                                                                                                                                                                                            16-DEC-1992
                                                                                                                                                                                                                                                                EP518313-A2
                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                             Hepatitis C
This sequence was encoded by the Hepatitis C
                                                                         N-PSDB;
                                                                                                                                                                                                                        11-JUN-1992;
                                                                                                                                      (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1098
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                                                                         1992-417213/51.
DB; AAQ32436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFKQKALAFASRGNHVAPTHYVTESDA 228
|: :||||||||:||||| 128
| QWMNRLIAFASRGNHVSPTHYVAESDA 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DASQAAPYIEQAQVI------AHQFKEKVLAFASRGNHDSPTHYVPESD 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVP-----ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPAIVPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKPAIIPDREVLYREFD-EMEESQHL-----PYIEQGMML----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AAP-----VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TASVTSPLTTQSTLLLNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA 1037
                                                                                                                 Honda Y,
                                                                                                                                                                                                                                                                                                                              virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
                                                                                                                                                         91JP-0172794.
91JP-0287008.
91JP-0332329.
92JP-0099957.
                                                                                                                                                                                                   91JP-0139268
                                                                                                                                                                                                                        92EP-0109812
                                                                                                                                                                                                                                                                                             Location/Qualifiers 2212
                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.2%;
                                                                                                                  Murakami
                                                                                                                                                                                                                                                                                     "Nonsense codon"
                                          and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 259; DB 14;
Pred. No. 5.6e-13;
                                                                                                                  Ή
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                         encoded protein - hepatitis C virus
                                                                                                                  Seki M,
                                                                                                                  Takahashi
   Virus
                                                                                                                                                                                                                                                                                                                                                                        NS1 (gp70); NS2-NS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
   (HCV)
                                                      used
                                            infections
   gene
                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
   of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -AE
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RESULT 12
AA: 56995
ID AAR66
XX
AC AAR66
XX
DT 01-AU
      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 96
AAQ74770 encodes AAR66995 the HC-J1/protein,
                                                  HCV genes and the corresponding proteins of anti-HCV antibodies and the detection
                         Claim 11; Pages 18-32; 35pp; Japanese.
                                                                                                                                                            10-DEC-1992;
                                                                                                                                                                                 10-DEC-1993;
                                                                                                                                                                                                             11-OCT-1994
                                                                                                                                                                                                                                        JP06284887-A
                                                                                                                                                                                                                                                                Hepatitis c
                                                                                                                                                                                                                                                                                                                 Hepatitis C virus gene
                                                                                                                                                                                                                                                                                                                                            01-AUG-1995
                                                                                                                                (IMMO ) IMMUNO JAPAN
                                                                                                                                                                                                                                                                                         Hepatitis C virus;
                                                                                                                                                                                                                                                                                                                                                                      AAR66995
                                                                                                                                                                                                                                                                                                                                                                                             AAR66995 standard; Protein; 3011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention. The HCV gene is useful in the development of a diagnostic method which is more accurate and effective than conventional ones, in the detection of antibodies raised against a wide range of HCVs which have been hardly detected before. The complete gene may be used in an in vitro screening system for a substance capable of specifically superessing or controlling a proteolytic processing of a precursor polypeptide of HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1788
                                                                                            1994-362594/45.
DB; AAQ74770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 30.3
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSPTHYVPESDAAARVT 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSPRHYVPESEPQVVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPGALVVGVVCAAILRRHVGPGEGAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRG------NHVAPTHYVVESDASASLPYMDETRAIAGQFKEKVLAFASRGNH 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVGAGITGAAVGSIGLGKVLVDILAGYGAGVAGALVAFK-VMSGDMPSTEDLVNLLPAIL 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLAEQFKQKALAFASRGNHVAPTHYVTESDAKPALVPDKEVLYQQYDEMEE-----AFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ASLMAFTASITSPLTTQYT-------LLFNILGGWVAAQLAPPSAASA 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHQFKEKVLAFASRGNHDSPTHYVPESDAKPAIIPDREVLYREFDEMEESQHLPYIEQGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQAQVI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPAVIPDREVLYQEFDEMBECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2510 AA;
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                          92JP-0360705
                                                                                                                                                                                 93JP-0345753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------VVESKWRALETFWAKHMWNFISGIQYLAGLSTLPGNPAI-----
                                                                                                                                                                                                                                                                                   HCV gene HC-J1/protein; specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%;
                                                                                                                                                                                                                                                                                                                HC-J1/protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259; DB 13;
No. 6.1e-13;

    used
    of HCV

 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                   in the production infection
 CDNA
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 can
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 used
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ARESULT 13
AAR12599
ID AAR12
XX AAR12
XX AAR12
XX DT 25-MA
DT 25-MA
DT 17-SE
XX POSt-
XX POST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSSSSS
SSSSX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                03-MAR-1990;
18-DEC-1989;
27-FEB-1990;
17-DEC-1990;
                                                           Claim 1; Page 88-97; 108pp; English.
                                                                                                           Post-transfusional non-A non-B hepatitis poly:peptide(s) also DNA and antibodies used in diagnostic assays and in
                                                                                                                                                                                     N-PSDB; AAQ12241.
                                                                                                                                                                                                              WPI; 1991-187584/26.
                                                                                                                                                                                                                                                             Highfield PE,
                                                                                                                                                                                                                                                                                                             (WELL )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-A, non-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Portion of PT-NANBH viral non-structural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB2239245-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      post-transfusional non-A, non-B hepatitis; virus; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
17-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR12599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR12599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the construction of an expression vector for the transformation of a host cell. The host cell can then be used in the production of proteins and peptides, useful in the preparation of monoclonal and polyclonal HCV-specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1691 RPALIPDREVLYREFDEMEECSQHLPYIEQGMMLAEQFKQKALGLLQTASRQAEVIAPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
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                                                                                                                                                                                                                                                                                                          WELLCOME F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VOWMNRLIAFASRGNHVSPTHYVPESDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQFKQKALAFASRGNHVAPTHYVTESDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTAAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGSGLAGAAVGSVGLGRVLVDIL 1852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPAVIPDREVLYQEFDEMEEAS-HLPYIEQGMQLAEQFKQKALAF---ASRQNHV-SPTH 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                90GB-0004814.
89GB-0028562.
90GB-0004414.
90GB-0027250.
                                                                                                                                                                                                                                                           Rodgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90GB-0027250
                                                                                                                                                                                                                                                                                                             FOUND
P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -IPDREVLYREFDEMEESQHL--PYIEQGMML-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.2%; Score 259; DB 15; 31.7%; Pred. No. 7.9e-13; cive 28; Mismatches 75;
                                                                                                                                                                                                                                                           BC,
                                                                                                                                                                                                                                                                                                                                 LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VQTNWQKLEAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMA 1792
                                                                                                                                                                                                                                                           Tedder RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1250
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                                                                                                                                                                                                                                                           Barbara JAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                             - and
vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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The sequence was deduced from a

non-structural (3') coding region humans infected by the PT-NANBH

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RESULT 14
AAR53417
ID AAR53
XX
AC AAR53
XX
T7-JA
XX
DT 17-JA
XX
XX
DE Blood
XX
XX
NANBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus. The polypeptide is an antigenic portion of the virus and will be useful in the development of vaccines for inducing immunity in man to PT-NANBH. The invention covers PT-NANBH viral polypeptides having an amino acid sequence at least 90 per cent homologous with the sequence given here, or antigenic fragments of such homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences.
See also AAQ12236-40 and AAQ12242.
(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                    Polymerase chain reaction; PCR; amplify; primer; non-A, NANBH; virus; blood transmissible; detection; hepatitis C100 antibody; HCV RNA; NS5 region.
                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                           Blood transmiscible NANBHV
                                                                                                                                                                                                                                                                             17-JAN-1995
                                                                                                                                                                                                                                                                                                                  AAR53417
                                                                                Misc-difference
                                                                                                  Misc-difference
                                                                                                                    Misc-difference
                                                                                                                                     Misc-difference
                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                    Non-A,
        Misc-difference
                                           Misc-difference
                                                              Misc-difference
                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 32.
                                                                                                                                                                                                     non-B hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPAIVPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTATKQAEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFKQKALAFASRGNHVAPTHYVTESDA
                                                                                                                                                                                                                                                                                                                                                                                                   GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                       TASVTSPLTTQSTLLLNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DASQAAPYIEQAQVI-------AHQFKEKVLAFASRGNHDSPTHYVPESD
                                                                                                                                                                                                                                                                                                                  standard; Protein; 3010 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    AKPAIIPDREVLYREFD-EMEESQHL----PYIEQGMML---
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                                                                                                                                                                         Location/Qualifiers
                                                                                                                                      246
                                              400
                                                                                                          /label= Asp,
                                                                                                                                              /label= Cys,
'label= Lys,
                                                                                         label=
                                                                                                                            'label= Leu,
                                                                                                                                                                'label= His,
                                                                     label= Gly,
                 label≖ Gln,
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                                   Thr,
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virus; RT-PCR;
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                             Blood-transmissible non-A non-B hepatitis detection of hepatitis virus
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                                                        WPI; 1994-163130/20
N-PSDB; AAQ63499.
                                                                                                                       10-MAR-1992;
                                                                                                                                                          JP06105690-A.
                                                                                                                                                                                                         Misc-difference
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            Claim
                                                                                                    10-MAR-1992;
                                                                                                                                          19-APR-1994
                                                                                   (KAEN/) KAENNO K.
           1; Page 8-20; 22pp; Japanese
                                                                                                     92JP-0051885
                                                                                                                       92JP-0051885
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Best Local
        New HCV-originated proteinase active substance site-specific cleavage by an intermolecular respurification thereof
                                                                          WPI; 1995-032330/05.
                                                                                                                                                                                   06-MAY-1993;
                                                                                                                                                                                                               15-NOV-1994.
                                                                                                                                                                                                                                         JP06315377-A
                                                                                                                                                                                                                                                                                                                        Hepatitis C
                                                                                                                                                                                                                                                                                                                                              proteinasé; serine; cleavage; hepatitis C virus; HCV
                                                                                                                                                                                                                                                                                                                                                                        HCV protein cleavable with new serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR68622;
                                                              N-PSDB; AAQ80498.
                                                                                                                                                         06-MAY-1593;
                                                                                                                                                                                                                                                                               Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR68622 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is encoded by the genome of a blood transmissible non-A, non-B hepatitis (NANBH) virus. The cDNA sequence was isolated using the primers given in AAQ63500-35. The amplified fragments are used in the detection of hepatitis virus. The target DNA was isolated from serum of chronically infected NANBH patients who were C100 antibody-positive and HCV RNA (NS5 region) positive. Reverse transcription-PCR and PCR were performed on cDNA and the total human NANBH DNA was constructed from 23 clones.
                                                                                                     (SUMQ)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                KAENNO K.
SOYAKU GIJUTSU KENKYUSHO KK
SUMITOMO METAL IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFKQKALAFASRGNHVAPTHYVTESDA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYGAGVAGALVAFKVMSGEAPSAEDLVNLLPAILSPGALVVXXVCAAILRRHVGPGEGAV 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TASITSPLTTONTLLENILGGWVAAQLAPPSAASXFVGAGIAGAAIGSIGLGKVLVDILA 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- AEAAAPVVESR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QWMNRLIAFASRGNHVSPTHYVPESDA 1940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Virus
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                                                                                                                                                        93JP-0105666
                                                                                                                                                                                   93JP-0105666
                                                                                                                                                                                                                                                                             Location/Qualifiers
2419..2420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.1%; Score 257; DB 15; 31.5%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                               "Serine protease cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---WRALEAFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
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                  reaction and
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                               This protein from HCV (hepatitis C virus) (encoded by AAQ80498) is cleaved between amino acids 2419 and 2420, by a new serine protease, contg. the sequence of AAR68621. The proteinase is purified as a fused product with the dihydrofolate reductase protein by using a methotrexate column. It can be used for the development of an inhibitor for HCV
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          proteinase.
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   1914
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                                                                                                                                                                                                                                                      1691 RPAVIPDREVLYQEFDEMEECASHLPY1QQGMQLAEQFKQKALGLLQTATKQAEA-----
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                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                          23 RPAVIPDREVLYQEFDEMEE-ASHLPYIEQGMQLAEQFKQKALAF---ASRQNHVSPTHY 78
                                                                                                                                                                                                                                                                                                                            85
'
                                                                                                                                                                                                                                                                                                                                        Similarity
QWMNRLIAFASRGNHVSPTHYVPESDA 1940
                            QFKQKALAFASRGNHVAPTHYVTESDA
                                                          GYGAGVAGALVAFKVMSGEMPSTEDLVNLLPAILSPGALVVGVVCAAILRRHVGPGEGAV 1913
                                                                                                                          TASITSPLTTQNTLLFNILGGWVAAQLAPPSAASAFVGAGIAGAAVGSIGLGKVLVDILA
                                                                                                                                                        -AQVIAHQFKEKVLAF-----ASRGNHDSPTHYVPESDAKPAI-----
                                                                                                                                                                                                                    VPESDARPAIIPDREVLHREFDEMEEAFASR-GNHVSPAHYVPESDASQAAPYIEQ----
                                                                                          ----PYIEQGMML----
                                                                                                                                                                                        -----AAP------VVESKWRALEVFWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAF 1793
                                                                                                                                                                                                                                                                                                                                                                                         3010 AA;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                        14.1%;
                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                       Score 257; DB 16;
Pred. No. 1.2e-12;
9; Mismatches 75;
                            228
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Search completed: July 25, 2003, 13:09:44
Job time: 87 secs